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(54) Title: GENE EXPRESSION PROFILES IN NORMAL AND CANCER CELLS (57) Abstract As a step towards understanding the complex differences between normal and cancer cells, gene expression patterns were examined in gastrointestinal tumors. More than 300,000 transcripts derived from at least 45,000 different genes were analyzed. Although extensive similarity was noted between the expression profiles, more than 500 transcripts that were expressed at significantly different levels in normal and neoplastic cells were identified. These data provide insights into the extent of expression differences underlying malignancy and reveal genes that are useful as diagnostic or prognostic markers.		

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Gene Expression Profiles in Normal and Cancer Cells

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TECHNICAL FIELD OF THE INVENTION

This invention is related to the diagnosis of cancer, and tools for carrying out such diagnosis.

BACKGROUND OF THE INVENTION

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Much of cancer research over the past 50 years has been devoted to the analyses of genes that are expressed differently in tumor cells compared to their normal counterparts. Although hundreds of studies have pointed out differences in the expression of one or a few genes, no comprehensive study of gene expression in the cancer cell has been reported. It is therefore not known how many genes are expressed differentially in tumor versus normal cells, whether the bulk of these differences are cell autonomous rather than being dependent on the tumor microenvironment, and whether most differences are cell-type specific or tumor specific. Thus there is a need in the art for information on the molecular changes that occur in cells during cancer development and progression.

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SUMMARY OF THE INVENTION

According to one embodiment of the invention, a method is provided for diagnosing colon cancer in a sample suspected of being neoplastic. The method comprises the steps of:

5 comparing the level of at least one transcript in a first sample of a tissue to a second sample, wherein the first sample is of a colonic tissue suspected of being neoplastic and the second sample is of a normal human colonic tissue, and wherein the transcript is identified by a tag selected from the group consisting of those shown in Table 3;

10 identifying the first sample as neoplastic when the level of the at least one transcript is found to be lower in the first sample than in the second sample.

 According to another embodiment of the invention, another method is provided for diagnosing colon cancer in a sample suspected of being neoplastic. The method comprises the steps of:

15 comparing the level of at least one transcript in a first sample of a tissue to a second sample, wherein the first sample is of a colonic tissue suspected of being neoplastic and the second sample is of a normal human colonic tissue, and wherein the transcript is identified by a tag selected from the group consisting of those shown in Table 2;

20 identifying the first sample as neoplastic when the level of the at least one transcript is found to be higher in the first sample than in the second sample.

25 In another embodiment of the invention an isolated and purified human nucleic acid molecule is provided. The molecule comprises a SAGE tag selected from SEQ ID NO:1-732.

30 In yet another aspect of the invention an isolated nucleotide probe is provided. The probe comprises at least 12 nucleotides of a human nucleic acid molecule, wherein the human nucleic acid molecule comprises a SAGE tag selected from SEQ ID NO: 1-732.

According to another aspect of the invention a method is provided for diagnosing pancreatic cancer in a sample suspected of being neoplastic. The method comprises the steps of:

5 comparing the level of at least one transcript in a first sample of a tissue to a second sample, wherein the first sample is of a pancreatic tissue suspected of being neoplastic and the second sample is of a normal human colon tissue, wherein said transcript is identified by a tag selected from the group consisting of those shown Table 4;

10 identifying the first sample as neoplastic when the level of the at least one transcript is found to be higher in the first sample than in the second sample.

According to still another embodiment of the invention a method of diagnosing cancer in a sample suspected of being neoplastic is provided. The method comprises the steps of:

15 comparing the level of at least one transcript in a first sample of a tissue to a second sample, wherein the first sample is of a tissue suspected of being neoplastic and the second sample is of a normal human tissue, wherein said transcript is identified by a tag selected from the group consisting of those shown Table 5;

20 identifying the first sample as neoplastic when the level of the at least one transcript is found to be higher in the first sample than in the second sample.

According to another embodiment of the invention a method is provided to aid in the determination of a prognosis for a colon cancer patient.

25 The method comprises the steps of:

 comparing the level of at least one transcript in a first sample of a tissue to a second sample, wherein the first sample is of a neoplastic colonic tissue and the second sample is of a normal human colonic tissue, and wherein the transcript is identified by a tag selected from the group consisting of those shown in Table 3;

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determining a poorer prognosis if the level of the at least one transcript is found to be lower in the first sample than in the second sample.

According to another aspect of the invention a method to aid in determining a prognosis for a patient with colon cancer is provided. The method comprises the steps of:

comparing the level of at least one transcript in a first tissue sample to a second sample, wherein the first sample is of a colonic cancer tissue and the second sample is of a normal human colonic tissue, and wherein the transcript is identified by a tag selected from the group consisting of those shown in Table 2;

determining a poorer prognosis if the level of the at least one transcript is found to be higher in the first sample than in the second sample.

In yet another embodiment of the invention a method is provided for diagnosing colon cancer in a sample suspected of being neoplastic. The method comprises the steps of:

comparing the level of expression of at least one protein in a first sample of a tissue to a second sample, wherein the first sample is of a colonic tissue suspected of being neoplastic and the second sample is of a normal human colonic tissue, and wherein the protein is encoded by a transcript identified by a tag selected from the group consisting of those shown in Table 3;

identifying the first sample as neoplastic when the level of expression of the protein is found to be lower in the first sample than in the second sample.

In another aspect of the invention a method of diagnosing colon cancer in a sample suspected of being neoplastic is provided. The method comprises the steps of:

comparing the level of expression of at least one protein in a first sample of a tissue to a second sample, wherein the first sample is of a colonic tissue suspected of being neoplastic and the second sample is of a normal human colonic tissue, and wherein the protein is encoded by a transcript

identified by a tag selected from the group consisting of those shown in Table 2;

identifying the first sample as neoplastic when expression of the protein is found to be higher in the first sample than in the second sample.

5 According to another embodiment of the invention a method is provided to aid in determining a prognosis of a patient having pancreatic cancer. The method comprises the steps of:

10 comparing the level of at least one transcript in a first sample of a tissue to a second sample, wherein the first sample is of a neoplastic pancreatic tissue and the second sample is of a normal human colon tissue, wherein said transcript is identified by a tag selected from the group consisting of those shown Table 4;

determining a poorer prognosis if transcription is found to be higher in the first sample than in the second sample.

15 In yet another aspect of the invention a method to aid in providing a prognosis for a cancer patient is provided. The method comprises the steps of:

20 comparing the level of at least one transcript in a first sample of a tissue to a second sample, wherein the first sample is of a neoplastic tissue and the second sample is of a normal human tissue of the same tissue type, wherein said transcript is identified by a tag selected from the group consisting of those shown Table 5;

determining a poorer prognosis if transcription is found to be higher in the first sample than in the second sample.

25 According to still another aspect of the invention, a method is provided for diagnosing pancreatic cancer in a sample suspected of being neoplastic. The method comprises the steps of:

30 comparing the level of expression of at least one protein encoded by a transcript in a first sample of a tissue to a second sample, wherein the first sample is of a pancreatic tissue suspected of being neoplastic and the second sample is of a normal human colon tissue, wherein said protein is

encoded by a transcript identified by a tag selected from the group consisting of those shown Table 4;

identifying the first sample as neoplastic when expression of the protein is found to be higher in the first sample than in the second sample.

5 According to yet another aspect of the invention a method is provided for diagnosing cancer in a sample suspected of being neoplastic. The method comprises the steps of:

10 comparing the level of expression of at least one protein in a first sample of a tissue to a second sample, wherein the first sample is of a tissue suspected of being neoplastic and the second sample is of a normal human tissue, wherein said protein is encoded by a transcript identified by a tag selected from the group consisting of those shown Table 5;

identifying the first sample as neoplastic when expression of the protein is found to be higher in the first sample than in the second sample.

15 In still another embodiment of the invention a method is provided to aid in the determination of a prognosis of a colon cancer patient. The method comprises the steps of:

20 comparing the level of expression of at least one protein in a first sample of a tissue to a second sample, wherein the first sample is of a neoplastic colonic tissue and the second sample is of a normal human colonic tissue, and wherein the protein is encoded by a transcript identified by a tag selected from the group consisting of those shown in Table 3;

determining a poorer prognosis if the level of expression is found to be lower in the first sample than in the second sample.

25 In still another embodiment of the invention a method is provided to aid in determining a prognosis for a patient with colon cancer. The method comprises the steps of:

30 comparing the level of expression of at least one protein in a first tissue sample to a second sample, wherein the first sample is of a colonic cancer tissue and the second sample is of a normal human colonic tissue, and

wherein the protein is encoded by a transcript identified by a tag selected from the group consisting of those shown in Table 2;

determining a poorer prognosis if the level of expression is found to be higher in the first sample than in the second sample.

5 In still another aspect of the invention a method is provided to aid in determining a prognosis of a patient having pancreatic cancer. The method comprises the steps of:

10 comparing the level of expression of at least one protein in a first sample of a tissue to a second sample, wherein the first sample is of a neoplastic pancreatic tissue and the second sample is of a normal human colon tissue, wherein said protein is encoded by a transcript identified by a tag selected from the group consisting of those shown Table 4;

determining a poorer prognosis if the level of expression is found to be higher in the first sample than in the second sample.

15 According to even a further aspect of the invention a method is provided to aid in providing a prognosis for a cancer patient. The method comprises the steps of:

20 comparing the level of expression of at least one protein in a first sample of a tissue to a second sample, wherein the first sample is of a neoplastic tissue and the second sample is of a normal human tissue of the same tissue type, wherein said protein is encoded by a transcript identified by a tag selected from the group consisting of those shown Table 5;

determining a poorer prognosis if the level of expression is found to be higher in the first sample than in the second sample.

25 In still another embodiment of the invention a method of treating a cancer cell is provided. The method comprises the step of:

30 administering to a cancer cell an antibody which specifically binds to a protein encoded by a transcript identified by a tag selected from the group consisting of those shown in Tables 2, 4, and 5, wherein the antibody is linked to a cytotoxic agent.

In another aspect of the invention an antibody linked to a cytotoxic agent is provided. The antibody specifically binds to a protein encoded by a transcript identified by a tag selected from the group consisting of those shown in Tables 2, 4, and 5.

5 According to another aspect of the invention, a method of detecting colon cancer in a patient is provided. The method comprises the steps of:

 comparing the level of at least one protein or transcript in a first body sample to a second body sample, wherein the first sample is a body sample of the patient and the second sample is of a normal human, wherein the
10 protein is encoded by a transcript and the transcript is identified by a tag selected from the group consisting of those shown in Table 2, wherein the first and second body sample is a sample selected from the group consisting of blood, urine, feces, sputum, and serum;

 identifying neoplasia when the level of the at least one protein
15 or transcript is found to be higher in the first sample than in the second sample.

In another aspect of the invention a method of detecting pancreatic cancer in a patient is provided. The method comprises the steps of:

 comparing the level of at least one protein or transcript encoded by a transcript in a first sample of a tissue to a second sample, wherein the first
20 sample is of the patient and the second sample is of a normal human, wherein said protein is encoded by a transcript and the transcript is identified by a tag selected from the group consisting of those shown Table 4, wherein the first and second sample is a sample selected from the group consisting of blood, urine, feces, sputum, and serum;

25 identifying neoplasia when the level of the at least one protein or transcript is found to be higher in the first sample than in the second sample.

Also provided by the present invention is a method of detecting cancer in a patient. The method comprises the steps of:

30 comparing the level of at least one protein or transcript in a first sample to a second sample, wherein the first sample is of patient and the second sample is of a normal human, wherein said protein is encoded by a

transcript and the transcript is identified by a tag selected from the group consisting of those shown Table 5, wherein the first and second body sample is a sample selected from the group consisting of blood, urine, feces, sputum, and serum;

5 identifying neoplasia when the level of the at least one protein or transcript is found to be higher in the first sample than in the second sample.

Additionally provided by the present invention is a method to aid in the determination of a prognosis for a colon cancer patient. The method comprises the steps of:

10 comparing the level of at least one protein or transcript in a first sample to a second sample, wherein the first sample is of a colon cancer patient and the second sample is of a normal human, wherein the protein is encoded by a transcript and the transcript is identified by a tag selected from the group consisting of those shown in Table 3, wherein the first and second body sample
15 is a sample selected from the group consisting of blood, urine, feces, sputum, and serum;

determining a poorer prognosis if the level of the at least one protein or transcript is found to be lower in the first sample than in the second sample.

20 Provided by another embodiment of the invention is a method to aid in determining a prognosis for a patient with colon cancer. The method comprises the steps of:

25 comparing the level of at least one protein or transcript in a first sample to a second sample, wherein the first sample is of a colonic cancer patient and the second sample is of a normal human, wherein the protein is encoded by a transcript and the transcript is identified by a tag selected from the group consisting of those shown in Table 2, wherein the first and second sample is a sample selected from the group consisting of blood, urine, feces, sputum, and serum;

determining a poorer prognosis if the level of the at least one protein or transcript is found to be higher in the first sample than in the second sample.

According to still another aspect of the invention, a method to aid in determining a prognosis of a patient having pancreatic cancer is provided. The method comprises the steps of:

comparing the level of at least one protein or transcript in a first sample to a second sample, wherein the first sample is of a pancreatic cancer patient and the second sample is of a normal human, wherein said protein is encoded by a transcript and the transcript is identified by a tag selected from the group consisting of those shown Table 4, wherein said first and second sample is a sample selected from the group consisting of blood, urine, feces, sputum, and serum;

determining a poorer prognosis if the level of the at least one protein or transcript is found to be higher in the first sample than in the second sample.

Also provided by the present invention is a method to aid in providing a prognosis for a cancer patient. The method comprises the steps of:

comparing the level of expression of at least one protein or transcript in a first sample to a second sample, wherein the first sample is of a cancer patient and the second sample is of a normal human, wherein said protein is encoded by a transcript and the transcript is identified by a tag selected from the group consisting of those shown Table 5, wherein the first and second sample is a sample selected from the group consisting of blood, urine, feces, sputum, and serum;

determining a poorer prognosis if the level of the at least one protein or transcript is found to be higher in the first sample than in the second sample.

The present invention further includes antisense oligonucleotides complementary in whole or in part to SEQ ID NOS:1-732.

This invention also provides a method for screening for candidate agents that modulate the expression of a polynucleotide selected from the group consisting of the polynucleotides in SEQ ID NOS.1-732 or their respective complements, by contacting a test agent with a pancreatic or colon cell and monitoring expression of the polynucleotide, wherein the test agent which modifies the expression of the polynucleotide is a candidate agent.

The present invention provides the art with new methods and reagents for diagnosing and prognosing cancers. In addition, some of the newly disclosed genes may play an important role in the development of cancers.

BRIEF DESCRIPTION OF THE DRAWINGS

Fig. 1. Comparison of expression patterns in colorectal cancers and normal colon epithelium. **(FIG. 1A)** A semi-logarithmic plot reveals 51 tags that were decreased more than 10 fold in primary CR cancer cells whereas 32 tags were increased more than 10 fold. 62,168 and 60,878 tags derived from normal colon epithelium and primary CR cancers, respectively, were used for this analysis. The relative expression of each transcript was determined by dividing the number of tags observed in tumor and normal tissue as indicated. To avoid division by 0, a tag value of 1 was used for any tag that was not detectable in one of the samples. These ratios were then rounded to the nearest integer and their distribution plotted on the abscissa. The number of genes displaying each ratio was plotted on the ordinate. Tu: CR tumors; NC: Normal colon. **(FIG. 1B and FIG. 1C)** Differentially expressed genes in colorectal cancers. The number of transcripts found to be differentially expressed ($P < 0.01$) are presented as Venn diagrams. Diagrams of transcripts that were decreased **(FIG. 1B)** or increased **(FIG. 1C)** in CR cancers compared to normal colon epithelium. Comparisons were between primary tumors and cells in culture as indicated.

Fig. 2. Northern blot analysis of genes differentially expressed in gastrointestinal neoplasia. Northern blot analysis was performed on total RNA (5 μ g isolated from primary CR carcinomas (T) and matching normal colon epithelium (N), or pancreatic carcinomas. The top panel in each case show an

example of the ethidium bromide stained gels prior to transfer. The number of SAGE tags observed in the original analysis is indicated to the right of each blot. (FIG. 2A) Examples of transcripts that were decreased or increased in CR cancers. (FIG. 2B) Examples of transcripts increased in pancreatic cancers (10). (FIG. 2C) Examples of transcripts elevated in cancer which were or were not cancer type specific. Probes used for Northern blot analysis were as follows (Human SAGE Tag unique identifier, gene name, (GenBank accession number)): (FIG. 2A) H204104, Guanylin (M95714); H259108, (see Table 2); H1000193, (see Table 2); H998030, (see Table 2). (FIG. 2B) H294155, RIG-E (U42376); H560056, TIMP-1 (S68252). (FIG. 2C) H802810, EST338411 (W52120); H85882, 1-8D (X57351); H618841, GA733-1 (X13425).

Tables 2-5. Transcripts Differentially Expressed in Human Cancer.

Tag sequence represents the NlaIII site plus the adjacent 11 bp SAGE tag. Tag number indicates a SAGE UID (unique identifier). NC, TU, CL, PT, PC, refers to the number of the indicated tag observed in RNA isolated from normal colorectal epithelium, primary colorectal cancers, colorectal cancer cell lines, primary pancreatic cancers, or pancreatic cancer cell lines, respectively. The Accession and Gene Name refer to representative GenBank entries that contain the tag sequence.

Table 2 Transcripts increased in colorectal cancer.

Table 3 Transcripts decreased in colorectal cancer.

Table 4 Transcripts increased in pancreatic cancer.

Table 5 Transcripts increased in pancreatic and colorectal cancer.

DETAILED DESCRIPTION

The inventors have discovered sets of human genes which are either upregulated or downregulated in cancer cells, as compared to normal cells. Specifically, certain genes have been found to be upregulated or downregulated in colorectal and/or pancreatic cancer cells, when compared to normal colon

cells. These sets of differentially regulated genes can be used as diagnostic markers, either individually or in sets of, for example, 2, 5, 10, 20, or 30.

Genes whose expression was detected to be increased in colorectal cancer are shown in Table 2. Genes whose expression was detected to be decreased in colorectal cancer are shown in Table 3. Genes whose expression was detected as increased in pancreatic cancer are shown in Table 4. Genes whose expression was detected as increased in both pancreatic cancer and colorectal cancer are shown in Table 5. These latter genes likely play a role in neoplastic development generally.

Tag sequences, as provided herein, uniquely identify genes. This is due to their length, and their specific location (3') in a gene from which they are drawn. The full length genes can be identified by matching the tag to a gene data base member, or by using the tag sequences as probes to physically isolate previously unidentified genes from cDNA libraries. The methods by which genes are isolated from libraries using DNA probes are well known in the art. See, for example, Veculescu et al., *Science* 270: 484 (1995), and Sambrook et al. (1989), *MOLECULAR CLONING: A LABORATORY MANUAL*, 2nd ed. (Cold Spring Harbor Press, Cold Spring Harbor, New York). Once a gene or transcript has been identified, either by matching to a data base entry, or by physically hybridizing to a cDNA molecule, the position of the hybridizing or matching region in the transcript can be determined. If the tag sequence is not in the 3' end, immediately adjacent to the restriction enzyme used to generate the SAGE tags, then a spurious match may have been made. Confirmation of the identity of a SAGE tag can be made by comparing transcription levels of the tag to that of the identified gene in certain cell types.

In addition to the sequences shown in SEQ ID NOS: 1-732, or their complements, this invention also provides the anti-sense polynucleotide stand, e.g. antisense RNA to these sequences or their complements. One can obtain an antisense RNA using the sequences provided in SEQ ID NOS: 1-732 and the methodology described in Vander Krol et al. (1988) *BioTechniques* 6:958.

The invention also encompasses polynucleotides which differ from that of the polynucleotides described above, but which produce the same phenotypic effect, such as the allele. These altered, but phenotypically equivalent polynucleotides are referred to "equivalent nucleic acids." This invention also encompasses polynucleotides characterized by changes in non-coding regions that do not alter the phenotype of the polypeptide produced therefrom when compared to the polynucleotide herein. This invention further encompasses polynucleotides, which hybridize to the polynucleotides of the subject invention under conditions of moderate or high stringency.

The polynucleotides can be conjugated to a detectable marker, e.g., an enzymatic label or a radioisotope for detection of nucleic acid and/or expression of the gene in a cell. A wide variety of appropriate detectable markers are known in the art, including fluorescent, radioactive, enzymatic or other ligands, such as avidin/biotin, which are capable of giving a detectable signal. In preferred embodiments, one will likely desire to employ a fluorescent label or an enzyme tag, such as urease, alkaline phosphatase or peroxidase, instead of radioactive or other environmental undesirable reagents. In the case of enzyme tags, colorimetric indicator substrates are known which can be employed to provide a means visible to the human eye or spectrophotometrically, to identify specific hybridization with complementary nucleic acid-containing samples. Briefly, this invention further provides a method for detecting a single-stranded polynucleotide identified by SEQ ID NOS.1-732 or its complement, by contacting target single-stranded polynucleotides with a labeled, single-stranded polynucleotide (a probe) which is at least 10 nucleotides of the complement of SEQ ID NOS: 1-732 (or the corresponding complement) under conditions permitting hybridization (preferably moderately stringent hybridization conditions) of complementary single-stranded polynucleotides, or more preferably, under highly stringent hybridization conditions. Hybridized polynucleotide pairs are separated from un-hybridized, single-stranded polynucleotides. The hybridized polynucleotide

pairs are detected using methods well known to those of skill in the art and set forth, for example, in Sambrook et al. (1989) *supra*.

The polynucleotides of this invention can be isolated using the technique described in the experimental section or replicated using PCR. The PCR technology is the subject matter of United States Patent Nos. 4,683,195, 4,800,159, 4,754,065, and 4,683,202 and described in PCR: The Polymerase Chain Reaction (Mullis et al. eds, Birkhauser Press, Boston (1994)) or MacPherson et al. (1991) and (1994), *supra*, and references cited therein. Alternatively, one of skill in the art can use the sequences provided herein and a commercial DNA synthesizer to replicate the DNA. Accordingly, this invention also provides a process for obtaining the polynucleotides of this invention by providing the linear sequence of the polynucleotide, nucleotides, appropriate primer molecules, chemicals such as enzymes and instructions for their replication and chemically replicating or linking the nucleotides in the proper orientation to obtain the polynucleotides. In a separate embodiment, these polynucleotides are further isolated. Still further, one of skill in the art can insert the polynucleotide into a suitable replication vector and insert the vector into a suitable host cell (procaryotic or eucaryotic) for replication and amplification. The DNA so amplified can be isolated from the cell by methods well known to those of skill in the art. A process for obtaining polynucleotides by this method is further provided herein as well as the polynucleotides so obtained.

RNA can be obtained by first inserting a DNA polynucleotide into a suitable host cell. The DNA can be inserted by any appropriate method, e.g., by the use of an appropriate gene delivery vector or by electroporation. When the cell replicates and the DNA is transcribed into RNA; the RNA can then be isolated using methods well known to those of skill in the art, for example, as set forth in Sambrook et al. (1989) *supra*. For instance, mRNA can be isolated using various lytic enzymes or chemical solutions according to the procedures set forth in Sambrook et al. (1989), *supra* or extracted by nucleic-acid-binding resins following the accompanying instructions provided by manufactures.

Polynucleotides having at least 10 nucleotides and exhibiting sequence complementarity or homology to SEQ ID NOS: 1-732 find utility as hybridization probes. In some aspects, the full coding sequence of the transcript, i.e., for SEQ ID NOS: 1-732, are known. Accordingly, any portion of the known sequences available in GenBank, or homologous sequences, can be used in the methods of this invention.

It is known in the art that a "perfectly matched" probe is not needed for a specific hybridization. Minor changes in probe sequence achieved by substitution, deletion or insertion of a small number of bases do not affect the hybridization specificity. In general, as much as 20% base-pair mismatch (when optimally aligned) can be tolerated. Preferably, a probe useful for detecting the aforementioned mRNA is at least about 80% identical to the homologous region of comparable size contained in the previously identified sequences identified by SEQ ID NOS:1-732, which correspond to previously characterized genes or SEQ ID NOS:1-732, which correspond to known ESTs. More preferably, the probe is 85% identical to the corresponding gene sequence after alignment of the homologous region; even more preferably, it exhibits 90% identity.

These probes can be used in radioassays (e.g. Southern and Northern blot analysis) to detect, prognose, diagnose or monitor various pancreatic or colon cells or tissue containing these cells. The probes also can be attached to a solid support or an array such as a chip for use in high throughput screening assays for the detection of expression of the gene corresponding to one or more polynucleotide(s) of this invention. Accordingly, this invention also provides at least one of the transcripts identified as SEQ ID NOS:1-732, or its complement, attached to a solid support for use in high throughput screens.

The total size of fragment, as well as the size of the complementary stretches, will depend on the intended use or application of the particular nucleic acid segment. Smaller fragments will generally find use in hybridization embodiments, wherein the length of the complementary region may be varied,

such as between about 10 and about 100 nucleotides, or even full length according to the complementary sequences one wishes to detect.

5 Nucleotide probes having complementary sequences over stretches greater than 10 nucleotides in length are generally preferred, so as to increase stability and selectivity of the hybrid, and thereby improving the specificity of particular hybrid molecules obtained. More preferably, one can design polynucleotides having gene-complementary stretches of more than 50 nucleotides in length, or even longer where desired. Such fragments may be readily prepared by, for example, directly synthesizing the fragment by
10 chemical means, by application of nucleic acid reproduction technology, such as the PCR technology with two priming oligonucleotides as described in U.S. Pat. No. 4,603,102 or by introducing selected sequences into recombinant vectors for recombinant production. A preferred probe is about 50-75 or more preferably, 50-100, nucleotides in length.

15 The polynucleotides of the present invention can serve as primers for the detection of genes or gene transcripts that are expressed in pancreatic or colon cells. In this context, amplification means any method employing a primer-dependent polymerase capable of replicating a target sequence with reasonable fidelity. Amplification may be carried out by natural or recombinant
20 DNA-polymerases such as T7 DNA polymerase, Klenow fragment of E.coli DNA polymerase, and reverse transcriptase.

A preferred amplification method is PCR. However, PCR conditions used for each reaction are empirically determined. A number of parameters influence the success of a reaction. Among them are annealing temperature
25 and time, extension time, Mg^{2+} ATP concentration, pH, and the relative concentration of primers, templates, and deoxyribonucleotides. After amplification, the resulting DNA fragments can be detected by agarose gel electrophoresis followed by visualization with ethidium bromide staining and ultraviolet illumination.

30 The invention further provides the isolated polynucleotide operatively linked to a promoter of RNA transcription, as well as other regulatory

sequences for replication and/or transient or stable expression of the DNA or RNA. As used herein, the term "operatively linked" means positioned in such a manner that the promoter will direct transcription of RNA off the DNA molecule. Examples of such promoters are SP6, T4 and T7. In certain
5 embodiments, cell-specific promoters are used for cell-specific expression of the inserted polynucleotide. Vectors which contain a promoter or a promoter/enhancer, with termination codons and selectable marker sequences, as well as a cloning site into which an inserted piece of DNA can be operatively linked to that promoter are well known in the art and commercially available.
10 For general methodology and cloning strategies, see Gene Expression Technology (Goeddel ed., Academic Press, Inc. (1991)) and references cited therein and Vectors: Essential Data Series (Gacesa and Ramji, eds., John Wiley & Sons, N.Y. (1994)), which contains maps, functional properties, commercial suppliers and a reference to GenEMBL accession numbers for various suitable
15 vectors. Preferable, these vectors are capable of transcribing RNA in vitro or in vivo.

Fragment of the sequences shown in SEQ ID NOS:1-732 or their respective complements also are encompassed by this invention, preferably at least 10 nucleotides and more preferably having at least 18 nucleotides. Larger
20 polynucleotides, e.g., cDNA or genomic DNA, which hybridize under moderate or stringent conditions to the polynucleotide sequences shown in SEQ ID NOS:1-732, or their respective complements, also are encompassed by this invention.

In one embodiment, these fragments are polynucleotides that encode
25 polypeptides or proteins having diagnostic and therapeutic utilities as described herein as well as probes to identify transcripts of the protein which may or may not be present. These nucleic acid fragments can be prepared, for example, by restriction enzyme digestion of the polynucleotide of SEQ ID NOS:1-732, or their complements, and then labeled with a detectable marker. Alternatively,
30 random fragments can be generated using nick translation of the molecule. For

methodology for the preparation and labeling of such fragments, see Sambrook et al., (1989) *supra*.

Expression vectors containing these nucleic acids are useful to obtain host vector systems to produce proteins and polypeptides. It is implied that these expression vectors must be replicable in the host organisms either as episomes or as an integral part of the chromosomal DNA. Suitable expression vectors include viral vectors, including adenoviruses, adeno-associated viruses, retroviruses, cosmids, etc. Adenoviral vectors are particularly useful for introducing genes into tissues *in vivo* because of their high levels of expression and efficient transformation of cells both *in vitro* and *in vivo*. When a nucleic acid is inserted into a suitable host cell, e.g., a procaryotic or a eucaryotic cell and the host cell replicates, the protein can be recombinantly produced. Suitable host cells will depend on the vector and can include mammalian cells, animal cells, human cells, simian cells, insect cells, yeast cells, and bacterial cells constructed using well known methods. See Sambrook et al. (1989) *supra*. In addition to the use of viral vector for insertion of exogenous nucleic acid into cells, the nucleic acid can be inserted into the host cell by methods well known in the art such as transformation for bacterial cells; transfection using calcium phosphate precipitation for mammalian cells; or DEAE-dextran; electroporation; or microinjection. See Sambrook et al. (1989) *supra* for this methodology. Thus, this invention also provides a host cell, e.g. a mammalian cell, an animal cell (rat or mouse), a human cell, or a procaryotic cell such as a bacterial cell, containing a polynucleotide encoding a protein or polypeptide or antibody.

When the vectors are used for gene therapy *in vivo* or *ex vivo*, a pharmaceutically acceptable vector is preferred, such as a replication-incompetent retroviral or adenoviral vector. Pharmaceutically acceptable vectors containing the nucleic acids of this invention can be further modified for transient or stable expression of the inserted polynucleotide. As used herein, the term "pharmaceutically acceptable vector" includes, but is not limited to, a vector or delivery vehicle having the ability to selectively target

and introduce the nucleic acid into dividing cells. An example of such a vector is a "replication-incompetent" vector defined by its inability to produce viral proteins, precluding spread of the vector in the infected host cell. An example of a replication-incompetent retroviral vector is LNL6 (Miller, A.D. et al. (1989) *BioTechniques* 7:980-990). The methodology of using replication-incompetent retroviruses for retroviral-mediated gene transfer of gene markers is well established (Correll et al. (1989) *PNAS USA* 86:8912; Bordignon (1989) *PNAS USA* 86:8912-52; Culver, K. (1991) *PNAS USA* 88:3155; and Rill, D.R. (1991) *Blood* 79(10):2694-700. Clinical investigations have shown that there are few or no adverse effects associated with the viral vectors, see Anderson (1992) *Science* 256:808-13.

Compositions containing the polynucleotides of this invention, in isolated form or contained within a vector or host cell are further provided herein. When these compositions are to be used pharmaceutically, they are combined with a pharmaceutically acceptable carrier.

This invention further encompasses genes, either genomic or cDNA, which code for a polypeptide or protein in the cell of interest. The genes specifically hybridize under moderate or stringent conditions to a polynucleotide identified by SEQ ID NOS: 1-732 or their respective complements. The process of identification of larger fragment or the full-length coding sequence to which the partial sequence depicted in SEQ ID NOS:1-732 hybridizes preferably involves the use of the methods and reagents provided in this invention, either singularly or in combination.

Five methods are disclosed herein which allows one of skill in the art to isolate the gene or cDNA corresponding to the transcripts of the invention.

RACE-PCR Technique

One method to isolate the gene or cDNA which code for a polypeptide or protein and which corresponds to a transcript of this invention, involves the 5'-RACE-PCR technique. In this technique, the poly-A mRNA that contains the coding sequence of particular interest is first identified by hybridization to

a sequence disclosed herein and then reverse transcribed with a 3'-primer comprising the sequence disclosed herein. The newly synthesized cDNA strand is then tagged with an anchor primer of a known sequence, which preferably contains a convenient cloning restriction site attached at the 5'end. The tagged cDNA is then amplified with the 3'-primer (or a nested primer sharing sequence homology to the internal sequences of the coding region) and the 5'-anchor primer. The amplification may be conducted under conditions of various levels of stringency to optimize the amplification specificity. 5'-RACE-PCR can be readily performed using commercial kits (available from, e.g., BRL Life Technologies Inc, Clontech) according to the manufacturer's instructions.

Identification of known genes or ESTs

In addition, databases exist that reduce the complexity of ESTs by assembling contiguous EST sequences into tentative genes. For example, TIGR has assembled human ESTs into a datable called THC for tentative human consensus sequences. The THC database allows for a more definitive assignment compared to ESTs alone. Software programs exist (give examples) that allow for assembling ESTs into contiguous sequences from any organism.

Isolation of cDNAs from a library by probing with the SAGE transcript or tag

Alternatively, mRNA from a sample preparation was used to construct cDNA library in the ZAP Express vector following the procedure described in Velculescu et al. (1997) Science 270:484. The ZAP Express cDNA synthesis kit (Stratagene) was used accordingly to the manufacturer's protocol. Plates containing 250 to 2000 plaques are hybridized as described in Rupert et al. (1988) Mol. Cell. Bio. 8:3104 to oligonucleotide probes with the same conditions previously described for standard probes except that the hybridization temperature is reduced to room temperature. Washes are performed in 6X standard-saline-citrate 0.1% SDS for 30 minutes at room temperature. The probes are labeled with ³²P-ATP through use of T4 polynucleotide kinase.

Table 2 - Transcripts increased in colon cancer

Transcripts increased in only colon primary tumors compared to normal colon (61 genes)

NC: Normal Colon

TU: Colon Primary Tumor

CL: Colon Cancer Cell Line

PT: Pancreatic Primary Tumor

PC: Pancreatic Cancer Cell Line

#	Tag Sequence	Tag Number	NC	TU	CL	PT	PC	Accession	Gene Name
1	CATGCACCTAAATGG	H285759	612	755	411	161	333	F15516	H.sapiens mitochondrial EST sequence (1-12) from
2	CATGTGATTTCACTT	H933704	452	595	235	80	314	U35430	Human cytochrome c oxidase subunit III (COIII) pse
3	CATGCCTGTAATCCC	H388150	433	549	380	443	197	Z70701	H.sapiens mRNA (fetal brain cDNA c2_11).
								X71347	H.sapiens HNF1-C mRNA.
								X71346	H.sapiens HNF1-B mRNA.
4	CATGCACTACTCACC	H291282	293	527	78	14	83	U09500	Human mitochondrial cytochrome b gene, partial cds
5	CATGGTGAAACCCCA(G)	H753750	392	517	389	453	194	X66785	H.sapiens mRNA for transacylase (DBT).
								X17648	Human mRNA for granulocyte-macrophage colony-stimu
								U09087	Human thymopoietin beta mRNA, complete cds.
								U09088	Human thymopoietin gamma mRNA, complete cds.
								U20770	Human metastasis suppressor (KAI1) mRNA, complete
6	CATGGGCTTTAGGGA	H687915	37	372	6	29	11	W15552	zb91h11.s1 Soares parathyroid tumor NblIPA Homo sap
								W32091	zc05d03.s1 Soares parathyroid tumor NblIPA Homo sap
								R62866	yil1d07.r1 Homo sapiens cDNA clone 138925 5'.
7	CATGACTTTCCAAA	H130369	32	272	32	23	20	X89839	H.sapiens mitochondrial DNA for loop attachment se
8	CATGTGGTGATGCA	H965434	53	271	6	30	5	T11555	A1486F Homo sapiens cDNA clone A1486 similar to Mi
9	CATGAGGGTGTTTC	H175872	26	218	7	20	10	T15773	IB1870 Homo sapiens cDNA 3'end similar to Human mi
10	CATGAGGTCAGGAGA(T)	H177315	93	213	113	148	58	X12544	Human mRNA for HLA class II DR-beta (HLA-DR B).
								S73483	phosphorylase kinase catalytic subunit PHKG2 homol
								X74301	H.sapiens mRNA for MHC class II transactivator.
11	CATGTGGCCAGGCT	H1025322	124	194	63	111	51	U28687	Human zinc finger containing protein ZNF157 (ZNF15
								U29119	Human leiomyoma LM-196.4 ectopic sequence from HMG
								U56236	Human Fc alpha receptor b mRNA, complete cds.
								W03751	za62h11.r1 Soares fetal liver spleen INFLS Homo sa
12	CATGATCAGCCCTC	H214616	97	186	17	41	49	W03770	za63f10.r1 Soares fetal liver spleen INFLS Homo sa

13	CATGGGGGTCAGGGG	H699691	37	170	11	16	9	W04748	za42f09.r1 Soares fetal liver spleen INFLS Homo sa
								T12078	A730R Homo sapiens cDNA clone A730 similar to Mito
14	CATGGCTAGGTTTAT	H641789	38	144	13	25	13	W45641	zc26a12.s1 Soares senescent fibroblasts NbHSF Homo
								D51017	Human fetal brain cDNA 3'-end GEN-007C04.
15	CATGCCCCGTACATC	H350996	56	132	35	0	18	D53694	Human fetal brain cDNA 3'-end GEN-117E01.
16	CATGAGTAGGTGGCC	H183018	18	131	2	17	7		Unknown
								D51021	Human fetal brain cDNA 3'-end GEN-007D07.
								D51052	Human fetal brain cDNA 3'-end GEN-009C05.
								D52836	Human fetal brain cDNA 3'-end GEN-089E01.
17	CATGCCTGTAGTCCC	H388278	79	124	61	71	23	D83195	Human DNA for Deoxyribonuclease I precursor.
18	CATGAGACCCACAAC	H136465	64	121	28	24	15	D54113	Human fetal brain cDNA 5'-end GEN-129B05.
19	CATGCATTGTATAA	H327364	49	107	35	7	40	F15796	H.sapiens mitochondrial EST sequence (102-25) from
20	CATGTCCCGTACCT	H874182	28	78	14	0	13		
21	CATGGCCCAACCTCCT	H606382	23	73	8	6	19	Z59183	H.sapiens CpG island DNA genomic MseI fragment, cl
								D52905	Human fetal brain cDNA 5'-end GEN-091D11.
22	CATGGCCATCCCCCTT	H609624	29	73	7	14	16	F16449	H.sapiens mitochondrial EST sequence (129-09) from
23	CATGTTGGTCAGGCT	H1027370	35	67	18	35	14	U06452	Human melanoma antigen recognized by T-cells (MART
24	CATGTCCTATTAAAG	H881603	20	49	17	15	26		
25	CATGTTACTTACT	H991026	2	47	2	1	4	D51004	Human fetal brain cDNA 3'-end GEN-006D02.
								L49057	Homo sapiens retinal fovea EST HFD010904 sequence.
								D51071	Human fetal brain cDNA 3'-end GEN-010E01.
26	CATGATGGCAGGAGT	H238755	13	45	1	4	2		
27	CATGCTAAGGCGAGG	H461411	5	44	2	3	3		
28	CATGGGTGAGACACT	H713234	7	44	20	13	15	J03592	Human ADP/ATP translocase mRNA, 3' end, clone pHAT
29	CATGACCTGTATCCC	H97078	6	42	17	100	32	X57352	Human 1-8U gene from interferon-inducible gene fam
30	CATGCCAGTCCGCCT	H339302	0	39	0	1	0	H01571	yj33e06.r1 Homo sapiens cDNA clone 150562 5' simil
								H03072	yj46g12.r1 Homo sapiens cDNA clone 151846 5' simil
31	CATGTAAATTTTGCC	H802810	1	37	0	1	0	T25155	EST730 Homo sapiens cDNA clone 34C11.
32	CATGTTAGCTTGTIT	H993264	6	37	2	3	5	D50972	Human fetal brain cDNA 3'-end GEN-004A05.
								D51211	Human fetal brain cDNA 3'-end GEN-017E08.
								D52162	Human fetal brain cDNA 3'-end GEN-069F04.
								T23865	seq2012 Homo sapiens cDNA clone Cot1374Ft-4HB3MA-3
33	CATGGCCACCCCTG	H607576	0	35	1	0	0	M32053	Human H19 RNA gene, complete cds.
34	CATGTAATAAAGGTG	H798764	13	35	19	33	51	X67247	H.sapiens rps8 gene for ribosomal protein S8.
35	CATGTACTGCTCGGA	H817627	13	35	5	1	14	T11939	A953F Homo sapiens cDNA clone A953 similar to Mito

36	CATGGTGAAACCCA	H753749	9	31	22	30	4	T95857	ye4201.s1 Homo sapiens cDNA clone 120409 3' simil
								W03237	za3509.r1 Soares fetal liver spleen INFLS Homo sa
								W03236	za6303.r1 Soares fetal liver spleen INFLS Homo sa
37	CATGGAACTGAACA	H526210	6	26	17	5	3	X54195	Human line-1 element DNA, host sequence flanking 1
								U29607	Human methionine aminopeptidase mRNA, complete cds
								H95100	yw57b10.r1 Homo sapiens cDNA clone 256315 5' simil
38	CATGACTTTTAAAA	H131009	1	22	4	1	0		Human keratinocyte cDNA, clone 067.
39	CATGACTCGTGCC	H555450	0	21	7	9	12	D29062	Human keratinocyte cDNA, clone 713.
								D29563	FB3B5 Homo sapiens cDNA clone FB3B5 3'end.
40	CATGTCAGTGGTAGT	H863923	4	21	2	2	1	T03196	H.sapiens CpG DNA, clone 164a10, reverse read cpg1
41	CATGAACTGTGTT	H7916	2	20	2	2	1	Z57093	H.sapiens CpG island DNA genomic MseI fragment, cl
								Z60184	H.sapiens CpG island DNA genomic MseI fragment, cl
								Z63649	H.sapiens CpG island DNA genomic MseI fragment, cl
								W31349	zb95d06.s1 Soares parathyroid tumor NbHPA Homo sap
42	CATGGGGGGGGGGT	H699051	0	19	0	0	0		zb96h01.s1 Soares parathyroid tumor NbHPA Homo sap
43	CATGGTGCCCGTGCC		2	19	1	0	0	W31448	zb96h01.s1 Soares parathyroid tumor NbHPA Homo sap
								W47282	zb96h01.s1 Soares parathyroid tumor NbHPA Homo sap
44	CATGGGGGGTAACTA	H699144	3	19	15	12	5	X71428	H.sapiens fus mRNA.
								S62140	TLS=translocated in liposarcoma [human, mRNA, 1824
								W31782	zb96a06.r1 Soares parathyroid tumor NbHPA Homo sap
								M24398	Human parathyrosin mRNA, complete cds.
45	CATGTCCTGCCCCAT	H883029	3	19	14	27	16		
46	CATGAAGTGCAAGA	H47683	0	16	0	0	0	U33317	Human defensin 6 (HD-6) gene, complete cds.
47	CATGGGTATTACCA	H708358	0	16	0	0	0	M98331	Homo sapiens defensin 6 mRNA, complete cds.
48	CATGGGCTACACCTT	H684312	2	16	0	2	1	D32027	Human mRNA for T cell receptor V beta 14 CDR3, par
			2	16	0	2	1	T11701	A1225F Homo sapiens cDNA clone A1225 similar to Mi
49	CATGAGGGTGTTC	H175870	1	15	0	0	0	D51783	Human fetal brain cDNA 5'-end GEN-051G02.
50	CATGCAAGGACGAC	H272467	0	13	0	2	0	D13138	Human mRNA for dipeptidase.
									Homo sapiens (clones MDP4, MDP7) microsomal dipept
									RDP=renal dipeptidase [human, kidney, Genomic, 357
51	CATGTGGAATGACC	H950498	0	13	0	167	0	M10629	Human alpha-1 collagen gene, 3' end with polyA sit
52	CATGATCCGCTGCC	H219514	1	13	3	4	1	H11641	ym17e04.s1 Homo sapiens cDNA clone 47962 3' simila
								R95667	yq51a09.s1 Homo sapiens cDNA clone 199288 3' simil
53	CATGTCCTGACAC	H875282	1	13	0	0	1		
54	CATGATGTAAAAAAT	H241665	0	11	0	12	14	M74090	Human TB2 gene mRNA, 3' end.

								J03801	Human lysozyme mRNA, complete cds with an Alu repe
								M19045	Human lysozyme mRNA, complete cds.
55	CATGCCAGCCCGTC	H337244	0	11	0	0	0		
56	CATGACCACTTCTGT	H85882	0	10	1	26	3	X57351	Human I-8D gene from interferon-inducible gene fam
								X02490	Human interferon-inducible mRNA (cDNA 1-8).
57	CATGAGGACCATCGC	H165175	0	10	0	0	0		
58	CATGATGGAAGAGT(A)	H243747	0	10	0	165	0	J03040	Human SPARC/osteonectin mRNA, complete cds.
59	CATGCAGTTGGTTGT	H310975	0	10	6	7	4	U55217	Human RNA fragment from patients with Crohn's dise
60	CATGGCCCTCTGCCA	H613862	0	10	2	15	7		
61	CATGTTAGATAAGCA	H992010	0	10	3	3	6	M94083	Human chaperonin-like protein (HTR3) mRNA, complet
								L27706	Human chaperonin protein (Tcp20) gene complete cds

Transcripts increased in both colon primary tumors and colon cancer cell lines compared to normal colon (47 genes)

NC: Normal Colon

TU: Colon Primary Tumor

CL: Colon Cancer Cell Line

PT: Pancreatic Primary Tumor

PC: Pancreatic Cancer Cell Line

#	Tag Sequence	Tag Number	NC	CT	CL	PT	PC	Accession	Gene Name
1	CATGGCAGCCATCCG	H599350	87	180	230	72	138	U14969	Human ribosomal protein L28 mRNA, complete cds.
2	CATGATGGCTGGTAT	H239533	52	153	318	80	294	X17206	Human mRNA for L1Rep3.
3	CATGCCCGTCCGAA	H355689	87	142	246	178	250	X64707	H.sapiens BBC1 mRNA
4	CATGAGGCTACGGAA	H171113	44	117	167	86	147	X56932	H.sapiens mRNA for 23 kD highly basic protein
5	CATGAGCACCTCCAG	H148949	42	116	197	103	190	Z11692	H.sapiens mRNA for elongation factor 2.
6	CATGCTGGGTAAATA	H502724	29	115	160	75	134	M81757	H.sapiens S19 ribosomal protein mRNA, complete cds
7	CATGGGATTGGCCT	H671654	55	108	222	73	185	M17887	Human acidic ribosomal phosphoprotein P2 mRNA, com
8	CATGTACCATCAATA	H807748	46	107	98	64	189	X53778	H.sapiens hng mRNA for uracil DNA glycosylase.
								J02642	Human glyceraldehyde 3-phosphate dehydrogenase mRNA
9	CATGTGGGCAAGCC	H959498	51	103	156	45	152	Z11531	H.sapiens mRNA for elongation factor-1-gamma.
								M55409	Human pancreatic tumor-related protein mRNA, 3' en
10	CATGAATCCTGTGGA	H55227	30	95	102	48	156	Z28407	H.sapiens mRNA for ribosomal protein L8.
11	CATGGACCACTGAA	H60601	36	92	114	43	63	X73460	H.sapiens mRNA for ribosomal protein L3.
12	CATGAGGGCTTCCAA	H174037	47	91	167	91	155	M73791	Human novel gene mRNA, complete cds.
								M64241	Human Wilms' tumor-related protein (QM) mRNA, comp
								S35960	laminin receptor homolog (3' region) [human, mRNA
13	CATGAAGGTGGAGGA	H44683	48	91	182	113	215	X80822	H.sapiens mRNA for ORF.
14	CATGTGCACGTTTTC	H935680	45	87	105	61	122	X03342	Human mRNA for ribosomal protein L32
15	CATGTCAGATCTTTG	H861056	37	81	93	50	92	M58458	Human ribosomal protein S4 (RPS4X) isoform mRNA, c
								M22146	Human scar protein mRNA, complete cds.
16	CATGTGGTGTGAGG	H965603	42	79	83	55	250	X69150	H.sapiens mRNA for ribosomal protein S18.
								L06432	Homo sapiens 18S ribosomal protein (HKE3) mRNA seq
17	CATGCCTAGCTGGAT	H379369	28	77	80	46	143	Y00052	Human mRNA for T-cell cyclophilin.
18	CATGCTGGGTTTTC	518912	0	73	42	0	0	X07868	Human DNA for insulin-like growth factor II (IGF-2);
19	CATGCTCCTCACCTG	H482584	12	72	41	34	50	U16811	Human Bak mRNA, complete cds.

20	CATGCTGTTGGTGAT	H507577	17	65	116	48	103	D14530	Human homolog of yeast ribosomal protein S28, comp
21	CATGCCGCGGAACAC	H416261	28	62	183	55	94	X73974	H.sapiens HRP4 mRNA.
22	CATGCAATAAATGTT	H274492	9	60	73	55	119	D23661	Human mRNA for ribosomal protein L37, complete cds
23	CATGACATCATCGAT	H79065	15	57	82	42	118	L06505	Human ribosomal protein L12 mRNA, complete cds.
24	CATGTTCAATAAAAA	H1000193	12	56	154	49	99	M17886	Human acidic ribosomal phosphoprotein P1 mRNA, com
25	CATGGAACACATCCA	H528694	24	56	71	24	146	X63527	H.sapiens mRNA for ribosomal protein L19.
26	CATGTTATGGGATCT	H998030	7	55	78	35	77	M24194	Human MHC protein homologous to chicken B complex
27	CATGGCATAATAGGT		18	53	50	19	61	U14967	Human ribosomal protein L21 mRNA, complete cds.
28	CATGATTCCTCCAGTA	H253260	23	50	103	49	120	X55954	Human mRNA for HL23 ribosomal protein homologue.
29	CATGACTCCAAAAA	H119809	15	49	64	21	64	X52839	Human mRNA for ribosomal protein L17.
30	CATGCTGTTGATTGC	H507455	9	44	54	22	40	X04347	Human liver mRNA fragment DNA binding protein UPI
31	CATGTACAAAATCGA	802871	0	42	20	0	0	X00910	Human mRNA for IGF-II precursor (insulin-like grow
32	CATGGAAAAATGGTT	H524524	14	41	81	15	57	X61156	H.sapiens mRNA for laminin-binding protein.
33	CATGAAGAAGATAGA	H33331	9	39	69	30	56	U02032	Human colon carcinoma laminin-binding protein mRNA
34	CATGCCTTCGAGATC	H390692	12	36	51	25	86	U14970	Human ribosomal protein L23a mRNA, partial cds.
35	CATGACTGGGTCTAT	H123661	5	29	25	25	38	X58965	Human ribosomal protein S5 mRNA, complete cds.
36	CATGCAGCTCACTGA	H302367	9	29	40	27	31	L10376	H.sapiens RNA for nm23-H2 gene.
37	CATGGTGTGTTGTA	H769020	0	24	15	22	8	M77349	Human putative NDP kinase (nm23-H2S) mRNA, complet
38	CATGGTGCCTGAGC	H760291	0	22	17	44	18	X58536	Homo sapiens c-myc transcription factor (puF) mRNA
39	CATGGTTTCACATTAG	H774461	3	22	25	141	10	X00497	Human (clone CTG-B33) mRNA sequence.
40	CATGTGAAATAAAAC	H918273	2	18	37	8	22	X16934	CAG-isl 7 (trinucleotide repeat-containing sequenc
41	CATGAAAAGAAACTT	H2056	1	16	27	11	25	Y00345	Human transforming growth factor-beta induced gene
42	CATGTGCTGCCTGTT	H948604	1	15	16	11	3	X81005	Human mRNA for HLA class I locus C heavy chain.
43	CATGCTGATGCGAGA	H495251	0	14	15	8	6	W46476	Human mRNA for HLA-DR antigens associated invarian
								X72718	Human hB23 gene for B23 nucleophosmin.
									Human mRNA for polyA binding protein.
									H.sapiens HCG IV mRNA.
									Human mRNA for BST-2, complete cds.
									Soares senescent fibroblasts NbHSF Homo sapiens cDNA clone
									324128 3'.
									H.sapiens DNA for orphan TCR V-beta segment (allele

44	CATGACTCGCTCTGT	H121311	0	12	16	5	7	H121311	Soares fetal heart NbHH19W Homo sapiens cDNA clone 342926
								AA305589	3' EST176663 Colon carcinoma (Caco-2) cell line II Homo sapiens cDNA 5' end
45	CATGCCCAAGGACC	H610466	0	12	19	82	17	X53416	Human mRNA for actin-binding protein (filamin) (AB
46	CATGATCTTGTTACT	H229106	0	11	28	67	0	X02761	Human mRNA for fibronectin (FN precursor).
47	CATGAAGCTGCTGGA	H40571	0	10	17	6	6	Z26305	H.sapiens isoform I gene for L-type calcium channe

Transcripts increased in only colon cancer cell lines compared to normal colon (181 genes)

NC: Normal Colon

TU: Colon Primary Tumor

CL: Colon Cancer Cell Line

PT: Pancreatic Primary Tumor

PC: Pancreatic Cancer Cell Line

#	Tag Sequence	Tag Number	NC	TU	CL	PT	PC	Accession	Gene Name
1	CATGTGTGTTGAGAG	H978825	71	79	487	136	412	X16869	Human mRNA for elongation factor 1-alpha
2	CATGGCCGAGGAAGG	H615043	72	66	265	105	125	X53505	Human ribosomal protein S12.
3	CATGCAAAACCATCCA	H263478	137	83	245	36	502	X12883	Human cytokeratin 18.
4	CATGCACAAACGGTA	H278636	63	53	201	74	179	L19739	Homo sapiens metalloproteinase (MPS1)
5	CATGAAAAAATAAAAA	H1	31	48	186	66	102	X83412	H.sapiens B1 mRNA for mucin.
								Z32564	H.sapiens FRGAMMA mRNA (819bp) for folate receptor
								X76180	H.sapiens mRNA for lung amiloride sensitive Na+ ch
								U08470	Human FR-gamma' mRNA, complete cds.
								U08471	Human folate receptor 3 mRNA, complete cds.
6	CATGTTGGTCTCTG	H1027448	115	128	179	104	358	S64030	Human L41 ribosomal protein
7	CATGTCCTCCATACCC	H906438	0	0	176	48	0	T91925	ye02f02.r1 Homo sapiens cDNA clone 116571 5'.
8	CATGAAGACAGTGGC	H33979	59	61	172	55	252	X66699	H.sapiens ribosomal protein L37a.
9	CATGCCGTCCAAAGGG	H374027	50	39	138	60	108	M60854	Human ribosomal protein S16
10	CATGGGGGAAATCGC	H696375	90	90	136	203	231	M92381	Human thymosin beta 10
11	CATGAAGGAGATGGG	H41531	30	37	133	38	161	X69181	H.sapiens mRNA for ribosomal protein L31.
12	CATGGAGGGAGTTTC	H567488	38	53	112	65	142	U14968	Human ribosomal protein L27a
13	CATGCCGTGGTTCCA	H424694	42	64	111	53	49	X79234	H.sapiens ribosomal protein L11.
14	CATGGCCGTGTCGGC	H618199	56	39	109	28	120	J03537	Human ribosomal protein S6
15	CATGGACGACACGAG	H549145	32	59	105	44	70	U58682	Human ribosomal protein S28 mRNA, complete cds
16	CATGTCACCCACACC	H857362	36	48	103	44	65	X52839	Human mRNA for ribosomal protein L17
17	CATGCCGCCCGGCT	H416106	39	43	90	52	184	U12465	Human ribosomal protein L35
18	CATGCTCAACATCTC	H475448	27	41	89	27	145	M17885	Human acidic ribosomal phosphoprotein P0
19	CATGTGGCCCAACCC	H955718	20	30	80	46	55	M23725	Human M2-type pyruvate kinase mRNA, complete cds.
								M26252	Human TCB gene encoding cytosolic thyroid hormone-
20	CATGCCCTGGGTTCT	H359102	34	49	78	92	145	M11147	Human ferritin L chain

21	CATGAGCATCTCCAG	H150997	0	0	77	0	0	H09058	y196f1.1 Homo sapiens cDNA clone 45943 5'
								Z44640	H. sapiens partial cDNA sequence; clone c-26605.
								N75111	yz29e01.1 Homo sapiens cDNA clone 284472 5'.
22	CATGCCCTGTATGAG	H621369	24	32	77	33	99	M31520	Human ribosomal protein S24 mRNA.
23	CATGAGCTCTCCCTG	H161624	33	39	76	21	67	X53777	Human L23 mRNA for putative ribosomal protein.
									gbIAA223340/AA223340 Homo sapiens cDNA clone 650651 3' similar to
24	CATGCCAGGAGGAAT	H338081	27	12	74	23	87	AA223340	gb:Y00371 ma1 HEAT SHOCK COGNATE 71 KD PROTEIN (HUMAN)
25	CATGGGCAAGCCCA	H672342	30	55	72	27	61	U12404	Human Csa-19
26	CATGAGGAAAGCTGC	H163999	31	42	70	32	146	F16378	H. sapiens EST sequence (135-18) from skeletal muscle
27	CATGAACGCGGCCAA	H26261	29	46	69	54	79	Z23063	Homo sapiens macrophage migration inhibitory factor
28	CATGCCAGAACAGAC	H335945	23	39	66	42	148	X79238	H. sapiens ribosomal protein L30.
29	CATGCCCGCATCTC	H615736	7	10	65	10	22	U55017	Human transketolase (TKT)
30	CATGGTGTAAACCAG	H769045	16	19	65	17	76	L25899	Human ribosomal protein L10
31	CATGCCTCGGAAAT	H383489	9	13	64	23	46	Z26876	H. sapiens ribosomal protein L38.
32	CATGAGGTCTAGCC	H177610	15	27	63	43	41	X06547	Human class Pi glutathione S-transferase
33	CATGGTCCCTGGCC	H775658	31	26	63	32	96	X65923	H. sapiens fau mRNA.
34	CATGTAAGGAGCTGA	H796831	32	58	62	42	68	X77770	H. sapiens RPS26
35	CATGAACATAAAAAA	H28673	7	14	60	17	39	W52460	ze45e1.1 Soares senescent fibroblasts NbHSF Homo
								N92893	2b71h03.s1 Homo sapiens cDNA clone 309077 3'.
36	CATGATTTGTCCAG	H260949	17	13	57	9	91	X14957	Human hmg1 mRNA for high mobility group protein I.
37	CATGATAATCTTTG	H200576	13	27	53	30	69	U14973	Human ribosomal protein S29
38	CATGCCCCAGCCAGT	H348756	18	23	53	5	85	U14990	Human XP1PO ribosomal protein S3 (pS3)
39	CATGGGAGTGGACAT	H667269	15	13	49	13	45	L11566	Homo sapiens ribosomal protein L18 (RPL18)
40	CATGTAAAAAATAAA	H786433	13	8	48	10	26	H08238	y187a01.1 Homo sapiens cDNA clone 44932 5'.
41	CATGGTGTGCACAA	H769605	19	21	48	21	47	X79239	H. sapiens ribosomal protein S13.
42	CATGCCAGCCAGC	H608595	6	21	47	11	15	U31657	Human unknown protein mRNA, partial cds.
								H41030	yu92a10.1 Homo sapiens cDNA clone 175866 5'.
43	CATGGGCTCCCACTG	H685384	14	24	47	23	15	M16660	Human 90-kDa heat-shock protein
44	CATGTCAACTTCTGG	H853983	0	0	46	2	0	N57419	yv82e04.1 Homo sapiens cDNA clone 258750 5' simil
45	CATGGATGCTGCCAA	H583573	6	12	46	27	18	X59357	Human mRNA for Epstein-Barr virus small RNAs (EBER)
								L21756	Homo sapiens acute myeloid leukemia associated protein
								D17652	Human mRNA for HBp15L22, complete cds.
46	CATGAATAGGTCCAA	H51925	13	31	46	47	53	M64716	Human ribosomal protein S25
47	CATGGCTTTAAGGA	H655115	8	26	45	22	63	L06498	Homo sapiens ribosomal protein S20 (RPS20)
48	CATGAATGCAGGCAG	H585533	2	12	44	6	27	M61831	Human S-adenosylhomocysteine hydrolase (AHCY)

49	CATGGCCAGCTGGA	H610939	8	18	43	0	22	Z21507	Human elongation factor 1 delta (EF 1delta)
50	CATGGCCGCGTTCC	H678334	6	6	42	8	18	M13932	Human ribosomal protein S17 mRNA
51	CATGTGAGGGAATAA	H928269	14	26	42	15	42	M10036	Human triosephosphate isomerase
52	CATGTGTACCTGTAA	H968173	14	24	42	35	49	K00558	human alpha-tubulin
53	CATGGGCAAGAGAA	H672265	8	7	41	12	87	L19527	Homo sapiens ribosomal protein L27 (RPL27)
54	CATGAACATAACAAA	H28737	6	14	40	14	15	X63237	H.sapiens Uba80 mRNA for ubiquitin.
55	CATGTATACGCTCAG	H837237	0	0	38	0	9		Unknown
56	CATGTACAAGAGGAA	H803369	7	17	38	14	42	X69391	H.sapiens ribosomal protein L6.
57	CATGGTTAACGTCC	H770486	8	17	38	12	25	H11182	ym14a02.r1 Homo sapiens cDNA clone 47866 5'
								T40302	ya31g04.r5 Homo sapiens cDNA clone 62262 5'
								T89480	yd98a05.r1 Homo sapiens cDNA clone 116240 5'
58	CATGGAGACTCCTGC	H558943	13	12	38	32	10	H01362	yi99c06.r1 Homo sapiens cDNA clone 147370 5'
59	CATGATCCACATCGC	H217399	3	10	37	10	14	H94371	yw54e05.r1 Homo sapiens cDNA clone 256064 5'
								T49412	ya75b09.r1 Homo sapiens cDNA clone 67481 5'
								T51058	yb53a12.r1 Homo sapiens cDNA clone 75070 5'
60	CATGGAAGCTTTGCA	H534522	11	13	37	14	25	X07270	Human heat shock protein hsp86.
61	CATGCTGGCGAGCGC	H501287	2	9	36	3	18	M91670	Human ubiquitin carrier protein (E2-EPF)
62	CATGCTGAGACAAAG	H493633	13	8	36	8	26	X74070	H.sapiens transcription factor BTF 3.
63	CATGAACGACCTCGT	H24951	7	13	35	22	40	V00599	Human beta-tubulin
64	CATGGCATAGGCTGC	H602783	9	16	35	2	17	X84694	H.sapiens mRNA for elongations factor Tu-mitochondria
								L38995	Homo sapiens nuclear-encoded mitochondrial elongation factor
								S75463	P43=mitochondrial elongation factor homolog (human
65	CATGCATCTTCACCA	H319302	12	14	35	9	16	H48893	yq80b12.r1 Homo sapiens cDNA clone 202079 5'
66	CATGGCCTGCTGGGC	H621035	10	5	32	18	107	X71973	H.sapiens GPx-4 mRNA for phospholipid hydroperoxidase
67	CATGACAGGCTACGG	H76231	0	5	31	64	0	M95787	Human 22kDa smooth muscle protein (SM22)
68	CATGGAAATGTAAGA	H528067	5	12	31	14	25	H80294	yu59g01.s1 Homo sapiens cDNA clone 230448 3'
								R74294	yi57f06.r1 Homo sapiens cDNA clone 143363 5'
69	CATGGAAGCCAGCCA	H533798	1	3	30	9	11	L36055	Human 4E-binding protein 1
70	CATGTTACCATATCA	H988366	10	28	30	19	86	F17005	H.sapiens EST sequence (011-T1-18) from skeletal muscle
71	CATGTTGCTCACAAA	H1023249	1	2	29	1	2	H10519	yi90g04.r1 Homo sapiens cDNA clone 45563 5'
72	CATGTCCCGCTCGA	H874103	0	6	29	0	0		Unknown
73	CATGATTAACAAGC	H246019	8	9	29	25	26	X04409	Human coupling protein G(s) alpha-subunit
74	CATGCAGATCTTTGT	H298495	2	7	28	8	24	X56998	Human Uba52 adrenal mRNA for ubiquitin-52 amino acid
75	CATGGTTGCTGCCAA	H777109	9	28	28	17	46	F19234	H.sapiens EST sequence (005-X3-16) from skeletal m
76	CATGGACGTGTGGGC	H552683	3	4	27	2	16	X52317	Human histone H2A.Z.

77	CATGCTAAAAA	H458753	4	8	27	19	8	M33680	Human 26-kDa cell surface protein TAPA-1
78	CATGGGGTTTTAT	H704500	4	1	27	6	18	L28809	Homo sapiens dbpB-like protein
79	CATGCCGATCACCGG	H363799	7	9	27	7	15	M29536	Human translational initiation factor 2 beta subunit
80	CATGGCACAAGAAGA	H594051	6	9	26	7	29	W07137	z92a1.l.r1 Soares fetal lung NbHL19W Homo sapiens
								D20503	Human HL60 3'directed Mbol cDNA, HUMGS01477, clone
								N91592	Soares fetal lung NbHL19W Homo sapiens cDNA clone 303055 3'.
								H83884	yv84c07.s1 Homo sapiens cDNA clone 249420 3' similar to contains Alu repetitive element.
81	CATGTCTCTACCCAC	H908373	7	11	26	11	13	Z22572	H.sapiens CDEI binding protein mRNA.
								L09209	Homo sapiens amyloid protein homologue mRNA, compl
								L19597	Human binding protein mRNA, partial cds.
								S60099	APPH=amyloid precursor protein homolog (human, pla
82	CATGGTTTCCCAAG	H783697	1	0	25	3	0	W07587	zb06f02.r1 Soares fetal lung NbHL19W Homo sapiens
								N28502	yx36f06.r1 Homo sapiens cDNA clone 263843 5'
								N35630	yx62a03.r1 Homo sapiens cDNA clone 266284 5'
83	CATGCCTGTCCAGCC	H388426	2	3	25	3	13	Z40265	H. sapiens partial cDNA sequence; clone c-1xe03.
								W02723	zc65c03.s1 Soares fetal heart NbHL19W Homo sapiens
								N24893	yx99h09.s1 Homo sapiens cDNA clone 269921 3'.
								N32178	yy25b09.s1 Homo sapiens cDNA clone 272249 3'.
84	CATGTCATCATCTGA	H865503	5	15	25	5	7	H21873	y134b10.s1 Homo sapiens cDNA clone 160123 3' simil
								H26394	y148e12.s1 Homo sapiens cDNA clone 161518 3' simil
								H69857	yr88d02.s1 Homo sapiens cDNA clone 212355 3' simil
								H70714	yu69b11.s1 Homo sapiens cDNA clone 239037 3' simil
85	CATGCCCTGCCCTTGT	H358783	5	8	25	16	31	X55110	Human mRNA for neurite outgrowth-promoting protein
86	CATGGCCGGGCCCTC	H617048	1	1	24	0	1	X03168	Human mRNA for S-protein.
87	CATGTTGCTCAAAAA	H1023233	2	1	24	2	2	AA143561	zo32d09.s1 Stratiagene colon (#937204) Homo sapiens cDNA clone 588593 3' similar to contains L.T.R7.1 L.T.R7 repetitive element
								AA152342	zo01g11.s1 Stratiagene colon (#937204) Homo sapiens cDNA clone 566468 3' similar to contains L.T.R7.1 L.T.R7 repetitive element ;
								AA115727	z186h11.s1 Stratiagene colon (#937204) Homo sapiens cDNA clone 511557 3' similar to contains L.T.R7.1 L.T.R7 repetitive element
88	CATGCAAAATCAGGA	H262987	6	2	24	5	15	R76502	yi61f09.r1 Homo sapiens cDNA clone 143753 5'.
								T32681	EST52915 Homo sapiens cDNA 5' end similar to None.
								T34662	EST72468 Homo sapiens cDNA 5' end similar to None.
89	CATGGAAGATGTGGG	H533435	1	5	23	4	7	H04634	yj49h03.r1 Homo sapiens cDNA clone 152117 5'.

117	CATGCGACCCACGC	H398663	2	6	17	48	0	M12529	Human apolipoprotein E
118	CATGTAGAAAAATAA	H819213	0	1	16	2	7	X16539	H.sapiens RNA for neuroleukin gene.
								M27691	Human transactivator protein (CREB) mRNA, complete
								M86667	H.sapiens NAP (nucleosome assembly protein)
119	CATGATCTTGAAAGG	H228867	0	0	16	5	3	X53743	H.sapiens mRNA for fibulin-1 C.
120	CATGCAGCTGGCCAT	H302741	0	1	16	14	0	Z26328	H.sapiens partial cDNA sequence; clone HEC059
121	CATGATCTTGAAAGG	H228867	0	0	16	5	3	Z26328	H.sapiens partial cDNA sequence; clone HEC059
121	CATGATCTTGAAAGG	H228867	0	0	16	5	3	Z26328	H.sapiens partial cDNA sequence; clone HEC059
122	CATGGTGGAGGTGGC	H762554	2	10	16	3	5	U22055	Human 100 kDa coactivator mRNA
123	CATGGTGGACCCAA	H762197	1	5	15	7	10	R91724	yp98e02.r1 Homo sapiens cDNA clone 195482 5' simil
								W51770	zc48a02.r1 Soares senescent fibroblasts NbHSF Homo
								N42086	yy05b03.r1 Homo sapiens cDNA clone 270317 5'
								R80990	y94c02.r1 Homo sapiens cDNA clone 146882 5'
124	CATGGAGCAGCTGGA	H561787	0	5	15	2	4	R95056	yq44f01.r1 Homo sapiens cDNA clone 198649 5' simil
								F16507	H.sapiens EST sequence (147-09) from skeletal musc
125	CATGGCGGGAGGGCT	H633002	1	6	15	8	7	T30201	yb77h05.r1 Homo sapiens cDNA clone 77241 5' simila
								S85655	Human prohibitin
126	CATGATTGGCTTAAA	H256497	1	8	15	0	16	M38188	Human unknown protein from clone pHGR74 mRNA, comp
127	CATGGAAAAATTAA	H524541	0	3	15	4	0	Y00711	Human lactate dehydrogenase B (LDH-B).
128	CATGGATCACAGTTT	H577840	0	5	15	0	0	D83174	Human collagen binding protein 2.
129	CATGAGCCTTTGTTG	H155632	1	2	15	23	5	X70940	H.sapiens elongation factor 1 alpha-2.
130	CATGCTGCACCTCC	H910430	0	0	15	0	2	T30623	EST19638 Homo sapiens cDNA 5' end similar to None.
131	CATGAACAGAAGCAA	H18469	0	2	15	3	11	C01011	HUMGS0004747, Human Gene Signature, 3'-directed cDNA sequence.
								zm62d06.s1	Stratagene fibroblast (#937212) Homo sapiens cDNA clone
								AA111865	530219 3'
								W56516	zdl6c08.r1 Soares fetal heart NbHH19W Homo sapiens
132	CATGTGTTTCAGGACC	H980130	1	1	14	5	11	H30299	yo77d04.r1 Homo sapiens cDNA clone 183943 5' simil
								H50265	yo28c02.r1 Homo sapiens cDNA clone 179234 5'.
133	CATGTAGATAATGGC	H822331	1	4	14	6	14	W01702	za37a06.r1 Soares fetal liver spleen INFLS Homo sa
								W04495	za58b10.r1 Soares fetal liver spleen INFLS Homo sa
								W23528	zc71g11.s1 Soares fetal heart NbHH19W Homo sapiens
134	CATGCTTAATCCTGA	H508767	0	6	14	6	12	D11838	Human HepG2 3'-directed Mbol cDNA, clone hm02e09.
135	CATGGGCAGAGGACC	H673954	0	6	14	5	11	X75598	H.sapiens nm23H1 gene.
136	CATGTGACTGAAGCC	H925194	0	5	14	3	0	T35470	EST85850 Homo sapiens cDNA 5' end similar to None.
								T35536	EST86951 Homo sapiens cDNA 5' end similar to None.

137	CATGGATAGTTGTGG	H576495	0	1	14	2	1	T35545	EST87066 Homo sapiens cDNA 5' end similar to None.
								H01694	yj33g1.s1 Homo sapiens cDNA clone 150596 3'.
								N78851	zb17d08.s1 Homo sapiens cDNA clone 302319 3'.
								N78931	za92h06.s1 Homo sapiens cDNA clone 300059 3'.
138	CATGGTGGTGGACAC	H765573	1	4	13	6	13	H90469	yy01e06.r1 Homo sapiens cDNA clone 241474 5' simil
								R76765	yic3g01.r1 Homo sapiens cDNA clone 143952 5' simil
								T35045	EST79335 Homo sapiens cDNA similar to None..
139	CATGTGGGTACCTT	H961304	0	6	13	2	9	H51447	yo31a05.r1 Homo sapiens cDNA clone 179504 5'.
								W46469	zc32c05.r1 Soares senescent fibroblasts NbHSF Homo
								W51800	zc48e04.r1 Soares senescent fibroblasts NbHSF Homo
								R33196	yh77f08.r1 Homo sapiens cDNA clone 135783 5'.
									Human prothymosin-alpha
140	CATGTTCAATTATAAT	H1003313	1	10	13	8	10	J04799	Human KIAA0190 protein
141	CATGCTCTGTGTAC(T)	H515821	0	5	13	8	12	D80012	Human tLON ATP-dependent protease mRNA
142	CATGACTGGCGAAGT	H125315	1	5	13	2	5	U02389	EST96617 Homo sapiens cDNA 5' end similar to ATP-d
								T29819	Human histone H2A.X.
143	CATGGAAGAGCTGA	H526495	1	3	13	1	6	X14850	Human DNA topoisomerase II (top2) mRNA
144	CATGCAACTCTATGG	H269775	0	1	13	1	2	J04088	Human beta globin retrovirus-like repetitive element
145	CATGAATTTGGTGC	H16303	0	0	13	0	0	K01891	EST28e05 Homo sapiens cDNA clone 28e05
								H88396	H.sapiens p85Mcm mRNA.
146	CATGCTGCACCTACT	H496114	1	2	13	1	8	X74796	Human mRNA for hMCM2, complete cds.
								D28480	Human B lymphoma mRNA for P1cd47, complete cds.
								D55716	EST14849 Homo sapiens cDNA 5' end similar to None.
147	CATGAATATTGAGAA	H53129	0	5	13	6	11	T30327	EST66942 Homo sapiens cDNA 5' end similar to None.
								T34394	yb14c03.r1 Homo sapiens cDNA clone 71140 5'.
								T47475	yb14b08.r1 Homo sapiens cDNA clone 71199 5'.
								T50289	Unknown
148	CATGTCGCGGGCGC	H890535	0	1	13	2	1		Unknown
149	CATGGGGGCAAGCCG	H697495	0	2	13	2	7	H59914	Human inducible poly(A)-binding protein
150	CATGCCAAGAAAGAA	H329737	0	6	12	4	4	U33818	Human HepG2 3' region cDNA, clone hmd2c11.
151	CATGTTTTTGATAAA	H1048113	0	5	12	4	12	D16891	Human apolipoprotein A-II
152	CATGTGTGGAGAGCC	H977034	0	0	12	0	0	M29882	H.sapiens mitoxanthrone-resistance associated mRNA.
153	CATGCCACGGTTAG	H345789	0	5	12	5	4	Z49216	Unknown
154	CATGAATTTCTCTAA	H63325	0	1	12	1	1		Unknown
155	CATGGACCTCCGGGC	H548203	0	0	12	0	0		Unknown
156	CATGTGAATCTGGGT	H921067	0	2	11	7	8	M93651	Human set gene

157	CATGTCCTTCTCCAC	H884181	0	5	11	14	8	X15804	Human alpha-actinin.
158	CATGTACTGTCTAC	H843485	0	4	11	2	3	T19569	609F Homo sapiens cDNA clone 609 similar to SET protein
159	CATGACGTTCTCTTC	H114144	0	0	11	1	17	Z36249	HHEA18W H. sapiens partial cDNA sequence; clone HEA18W;
160	CATGCCCTGAGTCAG	H358581	0	0	11	0	0	AA207189	zq73e07.r1 Stratagene neuroepithelium (#937231) Homo sapiens cDNA clone 647268 5' similar to TR:EI6910 EI6910 ENDONUCLEASE.;
161	CATGGAAATTCCTCGA	H540023	0	3	11	3	1	JN80776	za98h04.s1 Homo sapiens cDNA clone 300631 3'.
								AA025809	ze90d01.s1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 366241 3'.
								AA279492	zs85h05.s1 Soares NbHTGBC Homo sapiens cDNA clone 704313 3'.
162	CATGGACGCCGAAC	H550274	0	1	11	6	0		Unknown
163	CATGGCGGACTGGGG	H631275	0	0	11	1	0	AA098867	zk84f04.s1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 489535 3' similar to SW:A5 XENLA P28824 A5 PROTEIN PRECURSOR
164	CATGGGAACACACAG	H656453	0	1	11	0	2	R48460	yj67c12.r1 Homo sapiens cDNA clone 153814 5'.
								AA173819	zp01c02.r1 Stratagene ovarian cancer (#937219) Homo sapiens cDNA clone 595106 5'.
165	CATGTTGCGGAGCCC	H1022502	0	2	11	2	1	L19183	HUMMAC30X Human MAC30 mRNA, 3' end.
								H61710	yr24a07.s1 Homo sapiens cDNA clone 206196 3'.
								H77330	yu11f72.s1 Homo sapiens cDNA clone 233519 3'.
								N69482	zal8a05.s1 Homo sapiens cDNA clone 292905 3'.
166	CATGGCAGACATTGA	H598335	0	7	10	4	9	H41078	yp52c11.s1 Homo sapiens cDNA clone 191060 3' simil
167	CATGCACTTGAAAA	H294401	0	1	10	5	0	H04630	yy49g03.r1 Homo sapiens cDNA clone 152116 5'.
168	CATGGGTTGGCAGG	H719435	0	0	10	24	0	R77027	yj66e12.r1 Homo sapiens cDNA clone 144238 5'.
169	CATGTTCTCTCGGGC	H1007018	0	1	10	4	12	R32331	yh68g02.s1 Homo sapiens cDNA clone 134930 3' simil
170	CATGCTGCCGAGCT	-497192	0	8	10	1	10	T86566	yd77g07.r1 Homo sapiens cDNA clone 114300 5' simil
171	CATGGTGAAAAAAA	H753665	0	2	10	3	7	S77357	transcript chl11 [human, RFI, RF48 stomach cancer c
172	CATGCTGTGCAGCA	H506149	0	6	10	6	1	M34338	Human spermidine synthase
173	CATGTAGTTTGTGG	-835515	0	1	10	0	2	U03911	Human mutator gene (hMSH2)
174	CATGATGTAGTAGTG	H242380	0	5	10	9	7	D55671	Human heterogeneous nuclear ribonucleoprotein
175	CATGGACCACTACC	H545906	0	1	10	3	1	J03569	Human lymphocyte activation antigen 4F2 large subunit
176	CATGAAATAGGTTTT	H12992	0	1	10	6	3	D53402	Human fetal brain cDNA 5'-end GEN-108D03.
								T61971	yb96f02.r1 Homo sapiens cDNA clone 79035 5'.
								D61243	Human fetal brain cDNA 5'-end GEN-171G06.
								N77240	yy44d02.r1 Homo sapiens cDNA clone 245371 5'.
177	CATGCCGGCGTGGT	H371131	0	0	10	1	2	T35761	EST90898 Homo sapiens cDNA 5' end similar to EST c

178	CATGGACTGAGCTTG	H555168	0	8	10	3	3	T31901	EST40719 Homo sapiens cDNA 5' end similar to None.
179	CATGAAACGCCCAAT	H6481	0	2	10	1	3	X98264	U152336 H.sapiens mRNA for M-phase phosphoprotein, mpp4, 1523bp
180	CATGATGAGGCCGGG	H232027	0	4	10	7	1		Unknown
181	CATGGCCCCACATCCG(A)	H610614	0	9	10	6	2	D87433	Human mRNA for KIAA0246 gene, partial cds

Table 3 - Transcripts decreased in colon cancer

Transcripts decreased in only colon primary tumors compared to normal colon (51 genes)

NC: Normal Colon

TU: Colon Primary Tumor

CL: Colon Cancer Cell Line

PT: Pancreatic Primary Tumor

PC: Pancreatic Cancer Cell Line

#	Tag sequence	Tag Number	NC	CT	CL	PT	PC	Accession	Gene Name
1	CATGGCTTTATTGT	H654591	184	110	185	203	111	X00351	Human mRNA for beta-actin.
2	CATGCTAGCCTCACG	H468434	170	61	130	80	75	X04098	Human mRNA for cytoskeletal gamma-actin.
3	CATGCAAAACCATCCA	H263478	137	83	245	36	502	X12883	Human mRNA for cytokeratin 18.
4	CATGCTTCCAGCTAA	H513181	64	23	36	53	104	D00017	Human lipocortin II mRNA.
5	CATGCCCCAGTTGCT	H348922	61	27	38	37	46	X04106	Human mRNA for calcium dependent protease (small subunit)
6	CATGGATGACCCCC	H581974	53	4	42	6	32	Z65513	H.sapiens CpG island DNA genomic MseI fragment, cl
7	CATGCTGTACAGACA	H504098	50	22	26	6	32	W61077	zf30d02.r1 Soares fetal heart NbHL19W Homo sapiens
8	CATGGCGACTCACTG	H427848	47	15	26	18	4	D60944	Human fetal brain cDNA 5'-end GEN-141D02.
9	CATGCCCCCGCGGAA	H349801	47	10	21	15	8		Unknown
10	CATGCCCTGGAAGAGG	H387107	46	19	39	47	14	J02783	Human thyroid hormone binding protein (p55) mRNA.
11	CATGGCTGGCCATC	H621140	46	19	24	16	20	N33042	yy03d05.s1 Homo sapiens cDNA clone 270345 3'
12	CATGAGCAGGAGCAG	H150053	43	12	26	24	20	W07627	zb06a05.r1 Soares fetal lung NbHL19W Homo sapiens
13	CATGAACGTGCAGGG	H28235	42	6	57	2	10	X01630	Human mRNA for argininosuccinate synthetase.
14	CATGGCCGCCCTGCA	H615802	40	12	16	17	8	D43682	Human mRNA for very-long-chain acyl-CoA dehydrogen
15	CATGTGGGGAGAGGA	H960651	40	5	36	10	5	D29146	Human keratinocyte cDNA, clone 173.
16	CATGGCTGCCCTTGA	H648575	38	10	20	6	39	K00557	human alpha-tubulin mRNA, 3' end.
17	CATGTGGCCATCTGC	H955615	37	5	15	19	18	AA341633	AA341633 EST47188 Fetal kidney II Homo sapiens cDNA 5' end
18	CATGCGTTCCTGCGG	H456167	35	4	36	8	0	X77956	H.sapiens Id1 mRNA.
19	CATGTGCATCTGGTG	H937452	33	9	14	13	10	X87949	H.sapiens mRNA for BiP protein.
20	CATGGTGACCTCCTT	H755160	33	7	12	6	31	J04823	Human cytochrome c oxidase subunit VIII (COX8) mRNA
21	CATGTAGCTCTATGG	H826831	33	5	18	9	13	U16798	Human Na,K-ATPase alpha-I subunit mRNA, complete c
22	CATGGTGGCTAGGG	H760267	29	7	26	19	27	R50350	gbIR50350JR50350 yj59c04.s1 Homo sapiens cDNA clone 153030 3'.
								R50013	yj59c04.r1 Homo sapiens cDNA clone 153030 5'.
								C02981	Human Heart cDNA, clone 3NHC0642.

23	CATGGGGCGCTGTGG	H694767	28	6	20	6	26	T31329	EST30445 Homo sapiens cDNA 5' end similar to ubiquinol cytochrome-c reductase, 6.4 kDa.
24	CATGCCCTCCAGTAC	H382130	27	6	12	3	19		Unknown
25	CATGCTGTGACAGC	H388627	27	3	14	8	7	H63643	yc34d11.r1 Homo sapiens cDNA clone 207189 5' simil
26	CATGTCACAGTGCCT	H856806	24	5	8	17	11	W60924	zd27c08.r1 Soares fetal heart NbHH19W Homo sapiens
27	CATGAATAAAGGCTA	H49320	23	5	7	11	13	L25081	Human GTPase (rhoC) mRNA, complete cds.
28	CATGTTGTTGTGAA	H1031929	23	5	13	15	25	D45887	Human mRNA for calmodulin, complete cds.
29	CATGAAGGTAGCAGA	H44179	23	4	10	16	12	N62815	yy66b11.s1 Homo sapiens cDNA clone 278493 3'.
30	CATGTTGTTGGGGT	H769707	21	2	5	14	10	R68653	yi14b06.s1 Homo sapiens cDNA clone 139187 3'.
31	CATGTGCAGCGCCTG	H936344	21	1	5	7	13	X90858	H.sapiens mRNA for uridine phosphorylase.
32	CATGATGGCAGCGAG	H238697	20	2	4	0	3	H19458	yn54c02.s1 Homo sapiens cDNA clone 172226 3' simil
33	CATGGCCAGACACCC	H608326	20	1	6	1	9	T30468	EST17149 Homo sapiens cDNA 5' end similar to None.
34	CATGCTTCTTGCCCC	H515990	20	0	17	3	0	V00491	Human gene for alpha 1 globin.
35	CATGACCCACGTCAG	H86453	19	2	7	22	9	X51345	Human jun-B mRNA for JUN-B protein.
36	CATGGGCTGCCTGCC	H686458	18	3	4	5	8	R72429	yy90c08.s1 Homo sapiens cDNA clone 156038 3'.
								R48449	yy67b10.s1 Homo sapiens cDNA clone 153787 3'.
								R52128	yi72b03.s1 Homo sapiens cDNA clone 154253 3'.
37	CATGGAGGCGCGGTG	H567660	18	2	14	6	16	X12910	Human Na ⁺ /K ⁺ ATPase gene exons 1 - 3 (alpha III is
38	CATGGATGAATCCGG	H581847	17	1	3	2	2		Unknown
39	CATGAGCCCGACAC	H153109	16	2	11	7	5	X81006	H.sapiens HCG I mRNA.
40	CATGTTTCAGCTGTC	H774780	16	2	12	3	12	L08666	Homo sapiens porin (por) mRNA, complete cds and tr
41	CATGCCCTCGCTCAGT	H383443	16	1	8	6	7	U04627	Human 78 kDa gastrin-binding protein mRNA, complet
42	CATGCAAAATAAAAGT	H265219	15	1	8	9	0	U17077	Human BENE mRNA, partial cds.
43	CATGTGCGCGCCGCA	H940378	15	1	8	0	3	U28369	Human senaphorin V mRNA, complete cds.
44	CATGGCAGTGGCCTC	H601752	15	0	6	4	3	D12038	Human HepG2 3'-directed Mbol cDNA, clone sl50.
45	CATGCTGGGCTGAA	H502137	14	0	3	3	18	U77396	Human TNF-alpha inducible responsive element mRNA,
46	CATGGCCCAATTGGAG	H611305	13	1	6	13	17	Z29093	H.sapiens EDDR1 gene for receptor tyrosine kinase.
47	CATGAAGAAACCTC	H32792	12	0	2	2	0	T94990	yc38a04.s1 Homo sapiens cDNA clone 119982 3'.
								N69310	za25g05.s1 Homo sapiens cDNA clone 293624 3'.
									zb86e03.s1 Soares senescent fibroblasts NbHSF Homo sapiens cDNA
								N98502	clone 310492 3'
48	CATGGAATGATTCT	H538878	12	0	6	6	14	F18838	H.sapiens EST sequence (007-X1-01) from skeletal m
49	CA'GGCCTGGTCCTT	H621272	12	0	3	3	8	AA226928	zr21b10.s1 Stratagene NT2 neuronal precursor 937230 Homo sapiens
50	CCATGGCCCCACACAG	H610579	11	0	1	1	0	M60047	cDNA clone 664027 3'
									Human heparin binding protein (HBP17) mRNA

51	CATGGGATTCCAGTT	H671052	11	0	4	3	2	W52456	zc45e09.r1	Soares senescent fibroblasts NbHSF Homo
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										AA133597	512115.3	97 z192h02.s1 Stratagene colon (#937204) Homo sapiens cDNA clone
										T53199	ya86c05.s1 Homo sapiens cDNA clone 68552 3'	
										R00081	ye73c04.s1 Homo sapiens cDNA clone 123666 3'	
17	CTAGTGCTCTACCC	H947654	174	27	1	0	0			M16364	Human creatine kinase-B mRNA, complete cds.	
18	CATGCACCCCTGATG	H284132	172	33	26	3	6				yf22e12.s1 Homo sapiens cDNA clone 127630 3' similar to contains Alu repetitive element	
19	CATGCCGCTGCACTC	H368200	163	40	4	10	4			R09410	HUMGS0003915, Human Gene Signature, 3'-directed cDNA sequence.	
										C01918	yq04h09.s1 Homo sapiens cDNA clone 196001 3' similar to contains Alu repetitive element	
										R92735	zh78e12.s1 Soares fetal liver spleen INFLS S1 Homo sapiens cDNA clone 418222 3' similar to contains Alu repetitive element	
										W90374	H.sapiens pS2 protein gene.	
										X52003	Human prolactin receptor-associated protein (PRA)	
20	CATGCTGGCCCTCGG	H501111	163	20	0	26	1			M18981	Human galactoside-binding protein mRNA.	
21	CATGCCCCCTGGATC	H350116	160	40	24	88	181			M64303	Human mRNA for carcinoembryonic antigen pCEA80-11.	
22	CATGTTCACTGTGAG	H1001401	160	34	13	74	71			X16455	Human MHC antigen (HLA-B) mRNA, complete cds.	
23	CATGATTGGAGTGCT	H236186	155	34	1	11	6			U14943	Human calpactin 1 light chain mRNA, complete cds.	
24	CATGCTGACCTGTGT	H493039	149	44	32	98	37			M81457	HUMGS0002346, Human Gene Signature, 3'-directed cDNA sequence	
25	CATGAGCAGATCAGG	H149715	145	50	88	156	130			C21047	zo21h08.s1 Stratagene colon (#937204) Homo sapiens cDNA	
26	CATGGGAAACAGAA	H655433	126	37	0	24	16			AA132779	clone 587583 3' similar to SW:LEG4_RAT P38552 GALECTIN-4 cDNA	
										AA054072	z168h06.s1 Stratagene colon (#937204) Homo sapiens cDNA clone 509819 3'	
										AA132736	zo18g08.s1 Stratagene colon (#937204) Homo sapiens cDNA clone 587294 3' similar to SW:LEG4_RAT P38552 GALECTIN-4	
27	CATGTCACCGGTCAG	H857781	122	7	7	30	7			X04412	Human mRNA for plasma gelsolin.	
28	CATGTGCAGCACGAG	H936217	122	26	32	84	2			X77658	H. sapiens mRNA for HLA-B*7301.	
29	CATGGGAACTGTGAA	H657337	115	7	1	14	21			AA146606	zo35c09.s1 Stratagene colon (#937204) Homo sapiens cDNA clone 588880 3'	
										AA146775	zo35g09.s1 Stratagene colon (#937204) Homo sapiens cDNA clone 588928 3'	
										AA161043	zo74g11.s1 Stratagene pancreas (#937208) Homo sapiens cDNA clone 592676 3'	

[illegible]

[illegible]

									AA303091	EST12940 Uterus tumor 1 Homo sapiens cDNA 3' end za52d02.r1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone 296163 5'
63	CATGGCAGCTCCTGT	H599903	43	8	17	24	13		W02429	yx44c11.s1 Homo sapiens cDNA clone 264596 3'
									N20325	yz13c12.s1 Homo sapiens cDNA clone 282934 3'
									N45127	zb38c11.s1 Soares parathyroid tumor NbHPA Homo sapiens cDNA clone 305876 3'
									N90407	Human wild-type p53 activated fragment-1 (WAF1) mR zc11f01.s1 Soares parathyroid tumor NbHPA Homo sapiens cDNA clone 322009 3'
64	CATGTCCTCGTTC	H972720	43	12	14	25	5		U03106	gb1w15332 w15332 zc16d10.s1 Soares parathyroid tumor NbHPA Homo sapiens cDNA clone 322483 3'
65	CATGACAAAACCCCA	H65878	42	16	7	12	11		W37827	zc04g10.s1 Soares parathyroid tumor NbHPA Homo sapiens cDNA clone 321378 3'
									W15332	zw82c01.s1 Homo sapiens cDNA clone 258720 3'
									W32410	Human sodium/potassium-transporting ATPase beta-3 Unknown
									N32312	zp44f11.s1 Stratagene muscle 937209 Homo sapiens cDNA clone 612333 3' similar to contains Alu repetitive element;
66	CATGTAGGATGGGG	H828331	41	6	11	6	9		U51478	yh87e04.s1 Homo sapiens cDNA clone 136734 3' similar to contains Alu repetitive element.
67	CATGACTGTGGCGGC	H126619	41	7	1	4	35		R34696	zh87e04.s1 Homo sapiens cDNA clone 136734 3' similar to contains Alu repetitive element.
68	CATGGTAGCAGGTGT	H730287	40	7	13	17	24		AA180815	zq06e03.s1 Stratagene muscle 937209 Homo sapiens cDNA clone 628924 3' similar to contains Alu repetitive element
									AA194497	hbc760 Homo sapiens cDNA clone hbc760 3'end similar to nonspacific crossreacting antigen.
									T11144	zi67e01.s1 Stratagene colon (#937204) Homo sapiens cDNA clone 509688 3' similar to TR:G189087
69	CATGAATCACAAATA	H53508	40	12	0	3	0		AA058357	zo31e02.s1 Stratagene colon (#937204) Homo sapiens cDNA clone similar to none
									C05803	zp45b09.s1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone 585506 3'
									AA143765	612377 3'
70	CATGAGGATGGTCCC	H167606	40	11	4	4	5		AA179299	

	H328308	38	11	6	2	18	M35252	Human CO-029.
71	CATGCCAAAGCTATA						R87448	ym89c10.s1 Homo sapiens cDNA clone 166098 3'.
72	CATCGCGGAGTCGG	38	8	6	0	0	X79882	H. sapiens lrp mRNA.
73	CATGGCCGTGAGAG	38	9	5	17	26		Unknown
74	CATGCCCCCGAAGCC	37	6	0	0	0	J03037	Human carbonic anhydrase II mRNA, complete cds.
75	CATGATTCAAGATG	37	1	0	0	0		Unknown
76	CATGGCCAGTGGCT	37	3	0	2	10	M92843	H. sapiens zinc finger transcriptional regulator mRNA
77	CATGATCGTGCGGGA	36	2	6	25	2	X60188	Human ERK1 mRNA for protein serine/threonine kinase
78	CATGCCTGCCCCCCT	35	12	7	7	5	V01512	Human cellular oncogene c-fos (complete sequence).
79	CTAGTGGAAGTGAA	34	1	1	12	0	U34279	Human uroguanylin mRNA, complete cds.
80	CATGTCATCACAC	34	0	0	0	0		
81	CATGCTTATGGTCCC	34	1	0	3	1	AA287021	z57c03.s1 Soares NbHTGBC Homo sapiens cDNA clone 701572 3'
82	CATGCTGGGCCTCTG	34	3	4	11	5	T55226	yb47a01.s1 Homo sapiens cDNA clone 74280 3' containing L1 repetitive element
							R37446	yf56e10.s1 Homo sapiens cDNA clone 26129 3' similar to gb:X07173 INTER-ALPHA-TRYPsin INHIBITOR COMPLEX COMPONENT II
							AA406180	zu65c08.s1 Soares testis NHT Homo sapiens cDNA clone 742862 3'
							R09752	Unknown
83	CATGGCCCCAGGGCCC	33	3	0	0	2	R81530	yj02b10.r1 Homo sapiens cDNA clone 147547 5'.
84	CATGTTTTACTGAT	33	7	0	4	2	T32348	EST47211 Homo sapiens cDNA 3' end similar to None..
							zd17g02.s1	Soares fetal heart NbHH19W Homo sapiens cDNA clone 340946 3'
							w57810	
							zf47e12.s1	Soares ovary tumor NbHOT Homo sapiens cDNA clone 725518 3'
							AA398527	
85	CATGCCTGCTTGCTCG	32	2	1	6	32	X63187	H. sapiens HE4 mRNA for extracellular proteinase inhibitor homologue
86	CATGACCTGGGGAGG	32	6	4	8	6		Unknown
							yf52g07.s1	Homo sapiens cDNA clone 36232 3' similar to gb:M33987 CARBONIC ANHYDRASE I
87	CATGCCTTCAAATCA	31	1	0	0	0	R46266	
88	CATGTCGGAGCTGTT	30	1	4	7	1	H98618	yx12a06.s1 Homo sapiens cDNA clone 261490 3'.
							zo97h01.s1	Stratagene ovarian cancer (#937219) Homo sapiens cDNA clone 594865 3'
							AA171705	
							H99212	yx15g08.s1 Homo sapiens cDNA clone 261854 3'.

										AA029975	zk10e12.s1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 470158 3'
89	CATGGGAGGTGGGGC	H666539	30	6	5	32	22			M75161	H.sapiens granuln mRNA, complete cds.
90	CATGTTCCACTAAC	H1003970	30	7	3	16	17			T30344	gbIU53204HSU3204 Human plectin (PLEC1) mRNA, complete cds.
91	CATGGTCTGGGGGAT	H752297	29	1	3	9	3			T60135	yc22a06.s1 Homo sapiens cDNA clone 81394 3'
											gbJU67963HSU67963 Human lysophospholipase homolog (HU-K5)
										T30403	mRNA
											yh39a12.r1 Homo sapiens cDNA clone 132094 5' similar to gb:D26129
										R23595	RIBONUCLEASE PANCREATIC PRECURSOR (HUMAN)
92	CATGTTAACCCTCC	H984414	29	5	0	18	0				yj83c08.s1 Homo sapiens cDNA clone 155342 3' similar to gb:D26129
										R69445	RIBONUCLEASE PANCREATIC PRECURSOR (HUMAN);
											yi84h01.s1 Homo sapiens cDNA clone 145969 3' similar to gb:D26129
										R79191	RIBONUCLEASE PANCREATIC PRECURSOR (HUMAN);
											yj56c03.s1 Homo sapiens cDNA clone 152740 3' similar to gb:D26129
										R49965	RIBONUCLEASE PANCREATIC PRECURSOR (HUMAN);
											zv35h12.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone
											755687 5' similar to TR:G459890 G459890 OVEREXPRESSED IN
											TESTICULAR TUMORS
93	CATGATGACCTCAC	H231029	28	5	5	4	6			AA410947	Testicular tumor
										H02520	zoi2g08.r1 Stratiene colon (#937204) Homo sapiens cDNA clone
											586718 5' similar to TR:G459890 G459890 OVEREXPRESSED IN
										AA130551	TESTICULAR TUMORS.
											zd33c10.s1 Soares fetal heart NbHH19W Homo sapiens cDNA clone
											342450 3' similar to contains Alu repetitive element
										W68230	yp90a02.s1 Homo sapiens cDNA clone 194666 3' similar to contains Alu
94	CATGCACCTGTCATC	H286420	28	5	0	5	4				repetitive element;
										R89822	
											zk69e08.s1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone
										AA053322	488102 3' similar to contains element MER6 repetitive element
										V00594	Human mRNA for metallothionein from cadmium-treated cells
95	CATGGATCCCAACTG	H578824	27	1	1	24	17				yp21d05.r1 Homo sapiens cDNA clone 188073 5' similar to gb:J05021
										EZRIN	
96	CATGCTTAGAGGGGT	H510123	27	1	5	9	6			H43742	embY09610HSICE H.sapiens mRNA for putative carboxylesterase
97	CATGATGCCCATAC	H238925	27	4	3	1	0				Human messenger RNA for beta-globin.
98	CATGGCAAGAAAAGTG	H591884	27	1	0	2	0			V00497	

99	CATGTACCTCTGATT	H810468	27	5	7	11	12	X65614	H.sapiens mRNA for calcium-binding protein S100P.
100	CATGATGATGGCACC	H233106	26	0	2	0	2		embJZ6988 [HSSERCA3M H.sapiens mRNA for adenosine triphosphatase, calcium
101	CATGTTCTGTAGCCC	H1014566	25	5	0	4	0	T99568	ye65c02.r1 Homo sapiens cDNA clone 122594 5'.
102	CATGCCTGTCTGCCA	H388582	24	1	2	1	3	T87539	yd89f09.s1 Homo sapiens cDNA clone 115433 3'.
									gb AA347726 JAA347726 EST54132 Fetal heart II Homo sapiens cDNA 5' end similar to transmembrane secretory component
103	CATGTATGATGAGCA	H844682	23	4	0	1	0		Homo sapiens bone-derived growth factor (BPGF-I) m
104	CATGCTGGCAAAGGT	H500747	23	0	0	0	0	L42379	H.sapiens CL 100 mRNA for protein tyrosine phosphatase
105	CATGCTTGATTCCCA	H517078	23	4	4	17	7	X68277	Human N-benzoyl-L-tyrosyl-p-amino-benzoic acid hydrolase
106	CATGCTTGACATACC	H516402	22	0	0	7	2		alpha subunit (PPH alpha) mRNA, complete cds
107	CATGGCTGGCACATT	H649492	22	5	0	0	0	M82962	Human mRNA for transmembrane carcinoembryonic antigen (CEA)
108	CATGCTCTGAATTATG	H909556	21	1	1	1	1	X16354	H.sapiens mRNA for Gal-beta(1-3/1-4)GlcNAc alpha-2,3-sialyltransferase
109	CATGGGAAGAGCACT	H657554	21	1	1	3	3	X74570	yo45d01.s1 Homo sapiens cDNA clone 180865 3' similar to contains PTR5 repetitive element
110	CATGGCTCTTCCCA	H646998	20	2	0	1	0	R87768	yo36g07.s1 Homo sapiens cDNA clone 180060 3' similar to contains PTR5 repetitive element
								R85880	Human I-plastin mRNA, complete cds.
111	CATGAAATCTGGCAC	H114245	20	2	0	4	3	L20826	HSB4BMR H.sapiens mRNA for B4B
112	CATGTAATTGCAAT	H802708	19	2	0	1	7	Z50751	Human epithelial membrane protein (CL-20) mRNA, complete cds
								U77085	HSPAPR H.sapiens mRNA for Progression Associated Protein
								Y07909	EST10a24 Clontech adult human fat cell library HL1108A Homo sapiens cDNA clone 10a24.
113	CATGGTGGGGCGCC	H764570	18	1	1	8	2	R48529	yo45d01.s1 Homo sapiens cDNA clone 180865 3' similar to contains PTR5 repetitive element
114	CATGTTATGGTGTGA	H998127	17	0	0	1	0	T27534	sapiens cDNA clone 10a24.
115	CATGGGAGAAACAGC	H663571	17	1	2	4	0	T86124	yo45d04.s1 Homo sapiens cDNA clone 114895 3'.
								zo15g05.s1 Stratagene colon (#937204) Homo sapiens cDNA clone 10a24.	
								AA131008	587000 3'
								R49945	yo58g11.s1 Homo sapiens cDNA clone 152996 3'.
								T57044	yo84h01.s1 Homo sapiens cDNA clone 68401 3'.
116	CATGCCAACACACAGC	H328787	17	1	0	0	0		
117	CATGAGGTGACTGGG	H178299	17	0	0	0	0		
118	CATGGCCATCCTCCA	H609654	16	0	0	0	0		gb R73013 R73013 yj94a09.r1 Homo sapiens cDNA clone 156376 5'.

**Transcripts decreased in only colon cancer
cell lines compared to normal colon (78 genes)**

NC: Normal Colon

TU: Colon Primary Tumor

CL: Colon Cancer Cell Line

PT: Pancreatic Primary Tumor

PC: Pancreatic Cancer Cell Line

#	Tag sequence	Tag Number	NC	TU	CL	PT	PC	Accession	Gene Name
1	CATGCACCTAATTGG	H285759	612	755	411	161	333	F15516	H.sapiens mitochondrial EST sequence (1-t-12)
2	CATGATTTGAGAAGC	H260227	603	566	158	249	173	F12396	H. sapiens partial cDNA sequence; clone c-39e04.
3	CATGTGATTTCACCT	H933704	452	595	235	80	314	L08441	Human autonomously replicating sequence (ARS) mRNA
4	CATGTTTCATACACCT	H1002566	444	357	114	64	191	F15553	H.sapiens mitochondrial EST sequence (001T14)
5	CATGCCACTGCACCT	H335432	385	402	223	278	132	X51525	Human cortex mRNA containing an Alu repetitive element
6	CATGACTAACAACCT	H114966	369	446	171	76	161	F16402	H.sapiens mitochondrial EST sequence (141-20)
7	CATGCACTACTCACCT	H291282	293	527	78	14	83	U09500	Human mitochondrion cytochrome b gene, partial cds
8	CATGAAAACATTCTC	H1272	200	169	98	17	223	F15744	H.sapiens mitochondrial EST sequence (101-03)
9	CATGCTCATAAGGAA	H478249	184	127	70	21	75	F15511	H.sapiens mitochondrial EST sequence (1-t-07)
10	CATGTCGAAGCCGCC	H85334	147	183	94	49	57	F15587	H.sapiens mitochondrial EST sequence (022T19)
11	CATGACGCAGGGAGA	H103075	145	160	91	69	47	H03983	yy47a08.s1 Homo sapiens cDNA clone 151862 3'.
12	CATGTTGGCCAGGCT	H1023322	124	194	63	111	51	X74301	H.sapiens mRNA for MHC class II transactivator.
13	CATGTTGGTGAAGGA	H1027595	98	106	17	183	107	M17733	Human thymosin beta-4 mRNA, complete cds.
14	CATGATCACGCCCTC	H214616	97	186	17	41	49	U46913	Human EST overexpressed in pancreatic cancer (xs31)
15	CATGTGCTGCACCA	H941638	67	48	25	75	34	X05607	Human mRNA for cysteine proteinase inhibitor precursor
16	CATGAGACCCACAAC	H136465	64	121	28	24	15	D54113	Human fetal brain cDNA 5'-end GEN-129B05.
17	CATGAGTTTGTAGT	H196339	60	33	17	13	15	X14758	Human mRNA for adenocarcinoma-associated antigen
18	CATGGGAACAACAG	H656389	56	41	4	31	3	L33930	Homo sapiens CD24 signal transducer mRNA
19	CATGTGGTGTATGCA	H965434	53	271	6	30	5	D50954	Human fetal brain cDNA 3'-end GEN-002A10.
20	CATGGAATACAGTT	H527436	49	35	10	100	36	M11233	Human cathepsin D mRNA, complete cds.
21	CATGGTGGTTCACGC	H763719	49	37	21	27	15	U25801	Human Tax1 binding protein mRNA, partial cds.
22	CATGGTGGTGCACAC	H765509	45	26	18	23	15	U31215	Human metabotropic glutamate receptor 1 alpha
23	CATGGGGTTGGCTTG	H704160	44	56	2	6	1	S79597	tRNASer(UNC) [human, muscle, MERRF/MELAS overlap s
24	CATGGTGGCGGTGC	H763567	42	32	15	20	5	T48809	yb05c03.r1 Homo sapiens cDNA clone 70276 5' contai
25	CATGTAGACTAGCAA	H821029	39	23	1	23	10	M69023	Human globin gene.

[illegible]

										zo80f04.s1 Stratagene ovarian cancer (#937219) Homo sapiens cDNA clone 593215 3'	
										AA165679	
										zv40a02.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 756074 3'	
44	CATGTATAGTCCTCT	H838494	20	7	1	3	4			AA411012	
										z192g08.s1 Stratagene colon (#937204) Homo sapiens cDNA clone 512126 3'	
										AA133595	
										z56b12.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 726335 3'	
										AA292774	
45	CATGGTCTCTCTT	H710520	20	7	2	2	2			R53216	
46	CATGATGGCTTGAT	H240121	19	4	0	3	3			D20113	
47	CATGCTGCCCCCAT	H496981	19	5	0	1	4			Unknown	
48	CATGTTCTCTACACA	H1013522	19	4	1	8	2			U35048	
49	CATGAAGAAGCAGGG	H33355	18	4	2	2	8			R81767	
50	CATGAGTAGTGGCC	H183018	18	131	2	17	7			D51021	
51	CATGACAGTGTGT	H77551	18	5	3	0	8			D26146	
52	CATGGGAAAAAGTGGT	H655347	18	13	3	70	1			M11465	
53	CATGAAGAAAGCTC	H32926	17	4	0	5	1			R78188	
54	CATGACACCCATCAC	H70965	17	4	0	0	0			M22406	
55	CATGAGATCCCAAGG	H144707	17	18	0	0	0			T24507	
										N79237	
										T31354	
56	CATGAATAGTTCCC	H52214	16	4	0	0	0			H54696	
57	CATGCAGAAAGCATC	H295060	16	9	0	0	0			M22430	
58	CATGGCTTTGCTTG	H654976	16	4	2	8	1			AA374631	
										zn93g08.r1 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone 565790 5'	
										AA137163	
										zk10f05.s1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 470145 3'	
										AA029320	
59	CATGTCTGCATTGA	H948543	15	2	0	1	0			D25681	
										AA253331 3'	
										H05110	
60	CATGCCATCGTCCTT	H341720	15	8	1	1	10			Unknown	
61	CATGGAACAGCTCAC	H529013	14	23	0	0	0			EST112734 Colon I Homo sapiens cDNA 5' end	

										M2529	Human kallikrein mRNA, complete cds, clone p
62	CATGGGGCTACGTCC	H695406	14	4	0	1	0			H18836	ym45d10.s1 Homo sapiens cDNA clone 51262 3'
63	CATGCCCCGCTCCTC	H354776	14	7	1	5	2				zk01e10.s1 Soares pregnant uterus NBHPU Homo sapiens cDNA clone 469290 3'
										AA026974	zui2c12.r1 Soares testis NHT Homo sapiens cDNA clone 731638 5' similar to gb:M61900 Human prostaglandin D synthase gene, complete cds. (HUMAN); gb U66894 HSU66894 Human epithelium-restricted Ets protein ESX mRNA,
64	CATGAGGTACTACTA	H176584	13	9	0	9	8			U66894	Human epithelial-specific transcription factor ESE-1b (ESE-1) mRNA, complete cds
										U73843	Human colon 3'directed Mbol cDNA, HUMGS06772
65	CATGCAATAAATT	H265232	13	3	0	1	0			D25996	Unknown
66	CATGCTGTAAAAA	H503809	13	6	0	1	1				ze88g07.s1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 366108 3'
67	CATGGTTCAATCCCT	H774358	13	3	0	2	0			AA071520	za90h10.s1 Soares fetal lung NbHL19W Homo sapiens cDNA clone 299875 3'. zn52h06.s1 Stratagene muscle 937209 Homo sapiens cDNA clone 561851 3'
										N90742	Human HepG2 3'-directed Mbol cDNA, clone a-35.
										AA086292	IB2474 Homo sapiens cDNA 3'end.
68	CATGAATAAAGCCTT	H49304	12	4	0	0	0			D11499	yc82e01.r1 Homo sapiens cDNA clone 22306 5'.
69	CATGGGAAGGTTTAC	H658173	12	2	0	1	0			T16031	za61h02.s1 Homo sapiens cDNA clone 297075 3'. zh75f08.s1 Soares fetal liver spleen INFLS S1 Homo sapiens cDNA clone 417927 3'
70	CATGGGATGCCTTAT	H670333	12	1	0	6	1			T74426	H. sapiens partial cDNA sequence; clone c-29h08.
71	CATGGGTGCCCGGG	H715099	12	2	0	3	2			N73771	F03786
										W90388	Human 11 beta-hydroxysteroid dehydrogenase type II
										U14631	ya31a06.s5 Homo sapiens cDNA clone 62194 3' contains Alu repetitive element.
72	CATGTACTGTACTTC	H817952	12	2	0	0	0				T41121
											Unknown
73	CATGCCCCTTGCACTC	H360008	11	6	0	3	3				Unknown
74	CATGCGGTGGGACCA	H440966	11	4	0	2	0				Unknown
75	CATGCCCCCAACCA	H611590	11	2	0	0	0				Unknown
76	CATGCCCCGCGCTC	H618862	11	2	0	0	0			Z58486	Unknown
77	CATGGGAGGCGCTCA	H666014	11	1	0	0	0				Unknown

78	CATGTCCTCCCGTTACA	H874226	11	11	0	0	0	0	W68073	z442c12.s1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 343318 3' similar to contains Alu repetitive element;
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Table 4 - Transcripts increased in pancreas_cancer -
SAGE Tags elevated only in Pancreatic Tumor

NC: Normal Colon
 Tu: Colon Tumor
 CC: Colon Cancer Cell Line
 PT: Pancreatic Tumor
 PC: Pancreatic Cell Line

Tag Sequence	Tag Number	NC	Tu	CC	PT	PC	Examples	Accession	Gene Name
1 CATGAAAGCAACCA	H9222	0	6	1	3	11		R38305	yh95b04.s1 Homo sapiens cDNA clone 137455 3'
								AA126719	zk95b03.s1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 490541 3'
								AA044296	zk51g03.s1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 486340 3'
								AA131586	z133c08.s1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 503726 3'
								AA157983	zo71h12.s1 Stratagene pancreas (#937208) Homo sapiens cDNA clone 592391 3'
2 CATGAAAGCAGTTTA	H9408	1	5	2	21	3	Examples	AA292929	z154e04.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 726174 3'
								AA159306	zo78c07.s1 Stratagene pancreas (#937208) Homo sapiens cDNA clone 154129 3'
								R54012	yj70h01.s1 Homo sapiens cDNA clone 79335 3'
								T62936	y699f08.s1 Homo sapiens cDNA clone 79335 3'
								X52426	H. sapiens mRNA for cytokeratin 13
3 CATGAAAGCGGGCT	H9898	0	0	0	0	13	Examples	X51698	H.sapiens spasmodic polypeptide (SP) mRNA.
4 CATGAAATCCTGGGT	H13803	0	1	1	16	2	Examples	N70419	za61d12.s1 Homo sapiens cDNA clone 297047 3'
5 CATGAAATGGACAC	H14865	0	0	1	0	13	Examples	AA411599	zv16g01.r1 Soares NhHMPu S1 Homo sapiens cDNA clone 753840 5'
								AA410508	zv16g01.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 753840 3'
								AA115723	z186g12.s1 Stratagene colon (#937204) Homo sapiens cDNA clone 511558 3'
6 CATGAACCAAGTTGT	H21247	1	1	6	8	13	Examples	AA132875	zo19e04.s1 Stratagene colon (#937204) Homo sapiens cDNA clone 587358 3'
								AA147677	zo44a06.s1 Stratagene endothelial cell 937223 Homo sapiens cDNA clone 589714 3'

										AA206883							zq81h12.s1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone 648071 3'
7	CATGAACCTCTTGAAG	H30689	3	7	13	13	17	Examples	R51318 T35270								yq72f03.s1 Homo sapiens cDNA clone 38681 3' EST82235 Homo sapiens cDNA 3' end similar to None
																	zi65h12.s1 Soares testis NHT Homo sapiens cDNA clone 727271 3'
8	CATGAACCTGCTCAA	H31221	7	6	8	6	130	Examples	N63154 T87236 AA150720 AA045773								yz27f12.s1 Homo sapiens cDNA clone 285263 3' ye81h04.s1 Homo sapiens cDNA clone 22603 3' zl46f04.s1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 5049 zl68b12.s1 Stratagene colon (#937204) Homo sapiens
9	CATGAACCTGGCCAT	H32405	0	0	0	8	11	Examples	X07819 L22523								Human pump-1 mRNA homolog. to metalloproteinase, Human matrilysin gene, exon 5
10	CATGAAGATCCCCGC	H36183	5	10	14	12	23	Examples	R72650								yy95e05.s1 Homo sapiens cDNA clone 156512 3'
																	zd58e02.s1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 344858 3' similar to SW:CUTA_ECOLI P36654 PERPLASMIC DIVALENT CATION TOLERANCE PROTEIN CUTA
									W70287								yy95e05.s1 Homo sapiens cDNA clone 156512 3' similar to SP:CYCY_ECOLI P36654 C-TYPE CYTOCHROME BIOGENESIS PROTEIN CYCY
									R72650								zp61a11.s1 Stratagene endothelial cell 937223 Homo sapiens cDNA clone 624668 3' similar to SW:CUTA_ECOLI P36654 PERPLASMIC DIVALENT CATION TOLERANCE PROTEIN CUTA
									AA181976								Human phosphotyrosine independent ligand p62 for the Lck SH2 domain mRNA, complete cds
11	CATCAAGGCGAGGGTC	H43180	6	3	8	15	41	Examples	U46751								Human co-beta glucosidase (proactivator) mRNA
12	CATGAAGTTGCTATT	H48756	10	9	18	31	27	Examples	J03077								Human prosaposin (PSAP) gene
									M06181								Human sphingolipid activator proteins, mRNA
									D00422								Homo sapiens sphingolipid activator protein 1 mRNA
									J03015								Human mutant cerebroside sulfate activator protein
									M60255								
								No Match									
13	CATGAATGAAAAAA	H57345	0	1	5	2	10	Examples	N22375								yw37d01.s1 Homo sapiens cDNA clone 254401 3'
14	CATGACAAACTGTGG	H66031	17	4	24	5	60	Examples									zn20e01.s1 Stratagene neuroepithelium NT2RAM1 937234 Homo sapiens cDNA clone 547992 3'
									AA084643								

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23	CATGACTCAGCCCGG	H119383	0	0	3	21	3	Examples	M92357	Homo sapiens B94 protein mRNA, complete cds.
24	CATGACTGAGGAAG	H123521	0	0	0	53	22	Examples	X64875	H.sapiens mRNA for insulin-like growth factor binding protein 3
									M31159	Human growth hormone-dependent insulin-like growth factor binding protein 3
									M35878	Human insulin-like growth factor-binding protein-3
									S56205	insulin-like growth factor binding protein 3 (3' region)
25	CATGACTGCCCGCTG	H124264	1	0	0	22	9	Examples	U65932	Human extracellular matrix protein 1 (ECM1) mRNA
									U65937	Human extracellular matrix protein 1 (ECM1) gene, exon 9
26	CATGACTGTATTTTC	H126208	3	4	9	2	22	Examples	AA148916	zo03f09.s1 Stratagene colon (#937204) Homo sapiens cDNA clone 566633
									AA129137	zo12a11.s1 Stratagene colon (#937204) Homo sapiens cDNA clone 586652
									AA115437	z185g09.s1 Stratagene colon (#937204) Homo sapiens cDNA clone 511456
									AA126967	z187e07.s1 Stratagene colon (#937204) Homo sapiens cDNA clone 511620
27	CATGAGCACTGCAGC	H149395	1	2	6	3	16	Examples	R24613	yh36c03.r1 Homo sapiens cDNA clone 131812
28	CATGAGCAGAGCGT	H150055	1	0	0	0	15	Examples	H43243	yp05e05.r1 Homo sapiens cDNA clone 186560 5'
29	CATGAGCTGTATTCT	H162622	0	2	0	1	11	Examples	X54942	H.sapiens cks2 mRNA for Cks1 protein homologue
30	CATGAGGATGACCCC	H167446	1	7	12	10	13	Examples	AA044081	2k50g07.s1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 486300 3'
									AA044211	2k50g07.r1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 486300 5' similar to PIR:A40533 A40533 cAMP-dependent protein kinase major membrane substrate
31	CATGAGGTCTTCAAT	H178129	4	2	0	60	2	Examples	X14787	Class A, Human mRNA for thrombospondin.
32	CATGAGGTGCGGGG	H178603	0	2	2	1	11	Examples	R27738	yh64f11.s1 Homo sapiens cDNA clone 134541 3'
									H00276	yj22f12.s1 Homo sapiens cDNA clone 149519 3' similar to SP:ZK637.5
									CE00436	ARSA
33	CATGAGTATCTGGGA	H183787	3	3	1	15	73	Examples	AA076235	zm19d07.s1 Stratagene pancreas (#937208) Homo sapiens cDNA clone 526093 3'
									H13159	yj16c04.s1 Homo sapiens cDNA clone 148902 3'
									AA146632	zo71e11.s1 Stratagene pancreas (#937208) Homo sapiens cDNA clone 592364 3'
34	CATGATACTTTAATT	H204740	1	0	3	18	9	Examples	X80062	H.sapiens SA mRNA
									U01691	Human annexin V (ANX5) gene

									X12454	Human mRNA for vascular anticoagulant
									M18366	Human placental anticoagulant protein (PAP) mRNA
									M21731	Human lipocortin-V mRNA, complete cds
									J03745	Human endonexin II mRNA, complete cds
										GAMMA-INTERFERON-INDUCIBLE PROTEIN IP-30 PRECURSOR (HUMAN)
35	CATGATCAAGAATCC	H213518	2	1	5	25	1	Examples	J03909	EST97384 Thymus II Homo sapiens cDNA 3' end similar to interferon, gamma transducer 1
									aa383911	
36	CATGATCAAGGGTGT	H213679	12	9	25	12	156	Examples	U09953	Human ribosomal protein L9 mRNA
									U21138	Human ribosomal protein L9 mRNA, complete cds
									D14531	Human mRNA for human homologue of rat ribosomal protein
										znm3a05.s1 Stratagene corneal stroma (#937222) Homo sapiens cDNA clone 513008 3'
37	CATGATCAAGTTCGA	H213751	0	2	8	3	10	Examples	AA063259	
38	CATGATCCGGCGCCA	H219750	16	7	14	12	40	Examples	L42856	RNA polymerase II transcription factor SIII p18 subunit mRNA
39	CATGATGAAACTTCG	H229502	1	0	0	17	4	Examples	Z59242	H.sapiens CpG DNA, clone 13a10, reverse read cpgl
40	CATGATGCGGAAGGC	H235531	2	3	12	3	22	Examples	Z25820	H.sapiens mRNA for mitochondrial dodecenoyl-CoA dehydrogenase
									L24774	Homo sapiens delta3, delta2-CoA-isomerase mRNA
									M84711	40S RIBOSOMAL PROTEIN S3A (HUMAN)
41	CATGATGCTCTCGTT	H243676	0	0	1	0	14	Examples	M62403	Human insulin-like growth factor binding protein 4
42	CATGATGCTCTTCT	H243710	1	2	1	14	2	Examples		Human insulin-like growth factor binding protein-4 (IGFBP4) gene, promoter and complete cds
									U20982	
										H.sapiens msl gene.
43	CATGATGTGTAACGA	H244487	0	4	5	44	94	Examples	Z33457	Human CAPL protein mRNA, complete cds
									M80563	
44	CATGCAACTTAAGC	H270083	0	1	2	10	1	Examples	N23207	yx70b09.s1 Homo sapiens cDNA clone 267065 3' similar to gb:L12350 THROMBOSPONDIN 2 PRECURSOR (HUMAN)
45	CATGCACCTGTCCTT	H286424	0	4	2	10	1	Examples	AA285023	z125e11.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 714188 3' similar to gb:M33680 CD81 ANTIGEN (HUMAN)
									M33680	CD81 antigen
									D78203	Neurosin
46	CATGCACTCAATAAA	H291889	0	0	2	3	19	Examples	U62801	protease M

47	CATGCAGCCTGGGC	H300971	0	0	0	0	0	0	10	Examples	AA149942	zo68d04.s1 Stratagene pancreas (#937208) Homo sapiens cDNA clone 592039 3' similar to TR.E218488 E218488 TRYPTASE
48	CATGCAGCGCCCT	H301462	4	11	12	10	21			Examples	AA187553 M16937	zp66b09.r1 Stratagene endothelial cell 937223 Homo sapiens cDNA clone 625145 5' similar to gb:M16937 HOMEBOX PROTEIN HOX-B7 (HUMAN); contains element MER22 repetitive element Homeobox protein HOX-B7
49	CATGCAGGTTGCCT	H307126	0	0	4	0	10		No Match			Human ribosomal protein S10 mRNA
50	CATGCAGTCTCTCAA	H309109	2	6	6	2	17		Examples	U14972		Human leukotriene A4 hydrolase gene
51	CATGCATCCCGTGAC	H316857	0	3	3	3	13		Examples	U27293		Human leukotriene A-4 hydrolase mRNA, complete cds
										J03459		Human leukotriene A-4 hydrolase mRNA, complete cds
										J02959		H.sapiens mRNA for emerlin
52	CATGCATCCTCCTT	H325080	0	2	5	13	3		Examples	X82434		Human serum constituent protein (M5E55) mRNA
53	CATGCCACCCACCC	H333138	3	7	17	18	2		Examples	M88338		Human ribosomal protein S9 mRNA
54	CATGCCAGTGGCCCG	H339606	23	11	37	22	56		Examples	U14971		Homo sapiens alpha-1 type XV collagen mRNA
55	CATGCCATTTCTGG	H344031	0	2	6	1	10		Examples	L01697		Human mRNA for heat shock protein HSP27.
56	CATGCCCAAGCTAGC	H344691	19	8	8	18	44		Examples	X54079		H.sapiens mRNA for 28 kDa heat shock protein
										Z23090		Human mRNA fragment for estrogen-regulated 24k protein
										X16477		estrogen receptor-related protein=27-kDa heat shock protein
										S74571		H.sapiens mRNA for ribosomal protein L26.
57	CATGCCCATCCGAAA	H347489	20	15	43	19	61		Examples	X69392		Human ribosomal protein L26 (RPL26) gene
										L07287		Human mesothelin or CAK1 antigen precursor mRNA
58	CATGCCCCCTGCAGA	H350099	0	1	6	14	25		Examples	U40434		Human mRNA for pre-pro-megakaryocyte potentiating factor, complete cds.
										D49441		Human p16-INK4 (p16) gene
59	CATGCCCGCATAGAT	H353481	0	0	0	8	11		Examples	U12819		Human hypothetical 18.1 kDa protein (CDKN2A) mRNA
										U38945		MTS1= multiple tumor suppressor 1/cyclin-dependent kinase 4 inhibitor p16
										S69804		CDK41=cyclin-dependent kinase 4 inhibitor
										S69822		tumor suppressor gene, P16/MTS1/CDKN2=cell cycle negative regulator beta form
										S78535		
60	CATGCCCTCCTGGGG	H357867	8	2	5	14	34		Examples	Z47319		H.sapiens mRNA for expressed sequence tag (clone 21fi7119)

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[illegible]

									M73239	Human (clone SF1) hepatocyte growth factor (HGF)
									M73240	Human (clone SF2) hepatocyte growth factor (HGF)
110)	CATGGGAAAGTGGT	H655547	18	13	3	70	1	Examples	X02920	Human mRNA for alpha 1-antitrypsin carboxyterminal, 0
									X01683	Human mRNA for alpha 1-antitrypsin
									V00496	Human messenger RNA for alpha-1-antitrypsin
									J00067	Human alpha-1 antitrypsin gene, 3' end
111)	CATGGGAAGGGAGGC	H658059	0	0	4	6	16	Examples	AA127040	z122b01.s1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 502633 3'
									W81387	zdb6f06.s1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 347555 3'
									H45477	y072h08.s1 Homo sapiens cDNA clone 183519 3'
111	CATGGGAGTCATTGT	H666943	6	5	6	10	32	Examples	D26598	Human mRNA for proteasome subunit Hsc10-II, 0
112	CATGGGAGTGCGT	H667367	0	0	1	1	10	Examples	N74310	za78c01.s1 Homo sapiens cDNA clone 298656 3'
									H92750	y92e01.s1 Homo sapiens cDNA clone 231768 3'
									T24084	seq2272 Homo sapiens cDNA clone ssb4HB3MA(extended-ft-6) 3'
113	CATGGGATTGCTGG	H671455	3	7	13	5	21	Examples	X17567	H.sapiens RNA for snRNP protein B
									M34081	Human small nuclear ribonucleoprotein particle SmB
114	CATGGGCCCTCACC	H677330	0	0	2	9	22	Examples	M69054	Human insulin-like growth factor binding protein 6, 0
									M62402	Human insulin-like growth factor binding protein 6
115	CATGGGCCCTCTGAG	H677753	0	1	4	7	14	Examples	N74323	za78d08.s1 Homo sapiens cDNA clone 298671 3'
									H46766	y018t08.s1 Homo sapiens cDNA clone 178311 3'
									H41102	yn88a08.s1 Homo sapiens cDNA clone 175478 3'
									zn84b09.s1	Stratagene ovarian cancer (#937219) Homo sapiens cDNA clone 544601 3'
116	CATGGGCTGGTCTGG	H686815	0	1	3	13	22	Examples	AA074777	zm04g04.s1 Stratagene corneal stroma (#937222) Homo sapiens cDNA clone 513102 3'
									AA062735	zm63f12.s1 Stratagene fibroblast (#937212) Homo sapiens cDNA clone 530351 3'
									AA112905	
117	CATGGGAAGCAGAT	H688713	25	7	9	0	72	No Match		
118	CATGGGGAGGGTGG	H690863	2	3	1	16	2	No Match		
119	CATGGGGAGGTAGCA	H690890	1	0	1	14	1	No Match		
120	CATGGGGCATCTCTT	H693112	1	1	3	39	2	Examples	V00523	Human mRNA for histocompatibility antigen HLA-DR
									X00274	Human gene for HLA-DR alpha heavy chain a class II
									K01171	Human HLA-DR alpha-chain mRNA

121	CATGGGTGGGGAGAT	H715401	1	4	10	10	14	Examples	J00202 U18009	human hla-dr heavy chain gene; 3' flank
									U18009	Human chromosome 17q21 mRNA clone LF113.
									T33413	EST57778 Homo sapiens cDNA 3' end similar to None
									T33339	EST57474 Homo sapiens cDNA 3' end similar to None
122	CATGGTACTGTAGCA	H728778	3	3	1	16	30	Examples	M59911	Human integrin alpha-3 chain mRNA
123	CATGGTACTGTGGCT	H728810	23	10	16	15	50	Examples	X87689	H.sapiens mRNA for putative p64 CLCP protein
124	CATGGTCAAAATTTC	H737344	0	0	0	10	1	Examples	L12350	Human thrombospondin 2 (THBS2) mRNA
125	CATGGTCTGGGCTT	H752296	25	35	45	76	29	Examples	D21261	Human mRNA (HA1756) for ORF
									D29543	Human keratinocyte cDNA, clone 686
126	CATGGTCTGTGAGAG	H752521	0	5	7	12	2	Examples	H51290	yp07a05.s1 Homo sapiens cDNA clone 186704 3'
									N20338	yx44g12.s1 Homo sapiens cDNA clone 264646 3'
									AA158271	zo76s09.s1 Stralagene pancreas (#937208) Homo sapiens cDNA clone 592840 3'
127	CATGGTCTGTGCAGG	H752531	0	0	0	1	13	No Match		
128	CATGGTCTTGAAGCC	H753162	0	1	2	1	10	No Match		
129	CATGGTGAAGCAGT	H754323	25	14	42	15	89	Examples	X87373	Class C, H.sapiens RPS3a gene
130	CATGGTGAATGACGG	H754567	0	2	8	1	10	Examples	X08058	GLUTATHIONE S-TRANSFERASE P (HUMAN)
131	CATGGTGGGAGGAC	H760361	0	3	2	11	25	Examples	X51439	Human mRNA for serum amyloid A (SAA) protein
132	CATGGTGTGGAGAA	H761481	2	9	9	13	26	Examples	U15008	Human SnRNP core protein Sm D2 mRNA
133	CATGGTGGAGGCAC	H762533	1	1	3	6	34	Examples	U62800	Cystatin M (CST6)
134	CATGGTGGTACAGGA	H765003	14	17	15	39	30	Examples	H46430	yo12h12.s1 Homo sapiens cDNA clone 177767 3'
									AA047563	zfl3a06.s1 Soares fetal heart N6HH19W Homo sapiens cDNA clone 376786 3'
									AA130701	zo13f02.s1 Stralagene colon (#937204) Homo sapiens cDNA clone 586779 3'
135	CATGGTTCAGTCAG	H774629	0	2	1	13	3	Examples	X59288	H.sapiens gene for intercellular adhesion molecule
									M24283	Human major group rhinovirus receptor (HRV) mRNA
									J03132	Human intercellular adhesion molecule-1 (ICAM-1)
									M55100	Human cell surface glycoprotein P3.58 mRNA
136	CATGGTTGTCTTTGG	H781823	1	1	6	30	24	Examples	K02765	Human complement component C3 mRNA, alpha and beta
137	CATGGTTGTGTTAA	H782013	178	110	14	340	139	Examples	M17987	Human beta-2-microglobulin gene
138	CATGGTTTAAATCGA	H782391	1	6	12	4	14	Examples	D00760	Human mRNA for proteasome subunit HC3
139	CATGTAAGGCTTAAC	H797169	0	0	6	1	12	Examples	X57025	INSULIN-LIKE GROWTH FACTOR IA PRECURSOR (HUMAN)
140	CATGTAATTTTGGAA	H802793	0	2	5	2	10	No Match		

158	CATGTGATGTCTGGT	H932731	0	8	3	11	12	Examples	AA072860	2k05h07.s1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 469693 3'
159	CATGTGCCATCTGTA	H938876	1	3	7	3	16	Examples	M25753	G2MITOTIC-SPECIFIC CYCLIN B1 (HUMAN)
									T60151	yc22c04.s1 Homo sapiens cDNA clone 81414 3'
									R67969	yl29g08.s1 Homo sapiens cDNA clone 140702 3'
160	CATGTGCCCTCAAA	H939841	11	13	3	13	43	Examples	AA169614	zo91f03.s1 Stratagene ovarian cancer (#937219) Homo sapiens cDNA clone 594269 3' similar to SW:NGAL_HUMAN P80188 NEUTROPHIL GELATINASE-ASSOCIATED LIPOCALIN PRECURSOR
161	CATGTGCCCTCAGAA	H939849	3	4	0	11	19	Examples	N79823	zb15d08.s1 Homo sapiens cDNA clone 302127 3' similar to SW:NGAL_HUMAN P80188 NEUTROPHIL GELATINASE-ASSOCIATED LIPOCALIN PRECURSOR
162	CATGTGCCCTCAGGA	H939851	13	31	10	25	83	Examples	AA075896	zm90h04.s1 Stratagene ovarian cancer (#937219) Homo sapiens cDNA clone 545239 3' similar to SW:NGAL_HUMAN P80188 NEUTROPHIL GELATINASE-ASSOCIATED LIPOCALIN PRECURSOR
162	CATGTGCCCTCAGGC	H920392						No Match		
163	CATGTGCCCTTACTTT	H941856	0	3	1	2	12	Examples	AA100279	zl81e07.s1 Stratagene colon (#937204) Homo sapiens cDNA clone 511044 3'
164	CATGTGCGCTGGCCC	H944038	2	5	2	17	3	No Match		
165	CATGTGCTTCATCTG	H949560	2	6	6	4	16	Examples	AA029262	zk10a01.s1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 470088 3'
									N54281	yy66e10.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone 247722 3'
166	CATGTGGAGTGAGG	H953251	18	15	7	22	48	Examples	AA114075	zn76c02.s1 Stratagene NT2 neuronal precursor 937230 Homo sapiens cDNA clone 564098 3'
167	CATGTGCCCCAGGT	H955723	0	3	3	37	4	Examples	L76200	Homo sapiens guanylate kinase (GUK1) mRNA
168	CATGTGGGTGAGCCA	H962086	13	15	13	76	27	Examples	X00570	Human mRNA for precursor of apolipoprotein C1
									L16510	Homo sapiens cathepsin B mRNA
									M14221	Human cathepsin B proteinase mRNA, complete cds
169	CATGTGTGAGCCCT	H975446	3	3	3	22	8	Examples	L35240	Human enigma gene
170	CATGTGTGCTAATG	H976644	8	21	26	18	50	Examples	L38941	Homo sapiens ribosomal protein L34 (RPL34) mRNA
171	CATGTGTGTGTTGT	H978687	6	7	16	25	15	Examples	X03473	Human gene for histone H1(O)
172	CATGTTATGGATCTC	H997944	0	1	1	21	1	Examples	AA034505	zk23g08.s1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 471422 3'

										AA235464	z31b06.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 723923 3'
											z30c10.s1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 472050 3'
										AA037024	z30c10.s1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 472050 3'
										H53629	yz38d04.s1 Homo sapiens cDNA clone 236071 3'
										T06706	EST04595 Homo sapiens cDNA clone HFBDX32
											NIB1599 Normalized infant brain, Bento Soares Homo sapiens cDNA 3'end similar to EST04593 H. sapiens cDNA clone HFBDX32
										T16635	ze97h02.s1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 366963 3'
										AA026678	z05a03.s1 Soares NbHTGBC Homo sapiens cDNA clone 712204 3'
										AA280283	ym05a09.s1 Homo sapiens cDNA clone 46675 3'
										H10141	H. sapiens mRNA for tyrosine kinase receptor.
										X66029	Human mRNA for collagen VI alpha-1
										X15880	H. sapiens gene for glutamyl-IRNA synthetase
										X72414	z373h10.s1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 488515 3'
										AA044568	yz36b07.s1 Homo sapiens cDNA clone 285109 3'
										N71899	z371g03.s1 Soares testis NHT Homo sapiens cDNA clone 727828 3'
										AA400793	H. sapiens (5) Ferritin H pseudogene.
										X80336	Human mRNA for apoferritin H chain type
										X00318	Human apoferritin H gene exons 2-4
										X03488	Human ferritin heavy chain mRNA, complete cds
										M97164	Human ferritin heavy chain mRNA, complete cds
										L20941	Human interferon-inducible mRNA (cDNA 6-26).
										X02493	Human promyelocytic leukemia cell mRNA
										M11948	Human thymosin beta-4 mRNA, complete cds
										M17733	Human thymosin beta-4 mRNA, complete cds
										N78832	zb17a08.s1 Homo sapiens cDNA clone 302294 3'
										AA411095	z33d02.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 724131 3'
										W81693	z384g11.s1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 347396 3'

S1	CATGTTTCCTTCCTT	H1038296	0	6	3	7	17	Examples	M20471	Human brain-type clathrin light-chain A mRNA
									M20472	Human lymphocyte clathrin light-chain A mRNA
S2	CATGTTTGACCTTT	H1041504	2	0	0	16	1	Examples	X78947	H. sapiens mRNA for connective tissue growth factor
									U14750	Human connective tissue growth factor mRNA
S4	CATGTTTGTTAAA	H1044225							H06492	y178c08.s1 Homo sapiens cDNA clone 44773 3'
									T35952	EST94173 Homo sapiens cDNA 3' end similar to None
									AA23218	z553g10.s1 Soares NhlMPu S1 Homo sapiens cDNA clone 667170 3'

Table 5 - Transcripts increased in pancreas and colorectal cancer

SAGE tag that were elevated in both in colorectal and pancreatic tumor, and are likely to be specific for tumor in general.

Tag Sequence	Tag Number	Accession	Description
1 CATG TGGAAATGAC C	-950498	M10629	Human alpha-1 collagen gene, 3' end with polyA sit
2 CATG CACTCAAGG G	-294155	U42376	Human retinoic acid induced RIG-E precursor (E) mR
		U56145	Human thymic shared antigen-1/stem cell antigen-2
3 CATG ATGTGAAGAG T(A)	-243747	J03040	Human SPARC/osteonectin mRNA, complete cds.
		M25746	Human osteonectin gene exon 10, complete cds.
4 CATG GCCCAAGGAC C	-610466	X53416	Human mRNA for actin-binding protein (filamin) (AB
5 CATG ATCTTGTAC T	-229106	X02761	Human mRNA for fibronectin (FN precursor).
		K00799	human fibronectin (fn) 3' coding region and flank,
6 CATG GTGCGCTGAG C	-760291	X58536	Human mRNA for HLA class I locus C heavy chain.
		M26432	Human MHC class I HLA-C.1 gene, complete cds.
7 CATG ACAGGCTACG G	-76231	M95787	Human 22kDa smooth muscle protein (SM22) mRNA, com
		M83106	Human SM22 mRNA, 5' end.
8 CATG GTGTGTTTGT A	-769020	M77349	Human transforming growth factor-beta induced gene
9 CATG GATTCTCAG C	-589267	X53279	Human mRNA for placental-like alkaline phosphatase
		X55958	H.sapiens mRNA for alkaline phosphatase.
		J04948	Human alkaline phosphatase (ALP-1) mRNA, complete
10 CATG ACCATTCTGC T	-85882	X57351	Human 1-8D gene from interferon-inducible gene fam
		X02490	Human interferon-inducible mRNA (cDNA 1-8).
		X15804	Human mRNA for alpha-actinin.
11 CATG TCCTTCTCCA C	-884181	X15804	Human mRNA for KIRAO190 protein.
12 CATG CTTCTGTGTA C,T	-515821	D80012	Human mRNA for KIRAO190 protein.
13 CATG ATGTAAAAA T	-241665	M74090	Human TB2 gene mRNA, 3' end.
		J03801	Human lysozyme mRNA, complete cds with an Alu repe
		M19045	Human lysozyme mRNA, complete cds.
14 CATG GGCAGAGGAC C	-673954	X17620	Human mRNA for Nm23 protein, involved in developme
		X75598	H.sapiens nm23h1 gene.
15 CATG AATATTGAGA A	-53129	U62962	Human Int-6 mRNA, complete cds.
16 CATG TTTTGTATAA A	-1048113	D16891	Human HepG2 3' region cDNA, clone hmd2c11.
17 CATG CAGCTGGCCA T	-302741	X53743	H.sapiens mRNA for fibulin-1 C.

18	CATG GTTCACATTA	G	-774461	X00497	Human mRNA for HLA-DR antigens associated invariant
				M13560	Human Ia-associated invariant gamma-chain gene, ex
19	CATG AAAGAAACT	T	-2056	Y00345	Human mRNA for polyA binding protein.
20	CATG AATGCAGCA	G	-58533	M61831	Human S-adenosylhomocysteine hydrolase (AHCY) mRNA
				M61832	Human S-adenosylhomocysteine hydrolase (AHCY) mRNA
21	CATG TGAATAAAA	C	-918273	X16934	Human hB23 gene for B23 nucleophosmin.
				M28699	Homo sapiens nucleolar phosphoprotein B23 (NPM1) m
				M23613	Human nucleophosmin mRNA, complete cds.
				M26697	Human nucleolar protein (B23) mRNA, complete cds.
22	CATG TTATGGGATC	T	-998030	M24194	Human MHC protein homologous to chicken B complex
23	CATG CAATRAATGT	T	-274492	D23661	Human mRNA for ribosomal protein L37, complete cds
				L11567	Homo sapiens ribosomal protein L37 mRNA, complete
24	CATG AGCCTTTGTT	G	-155632	D83174	Human mRNA for collagen binding protein 2.
25	CATG ACCTGTATCC	C	-97078	X57352	Human 1-8U gene from interferon-inducible gene fam
26	CATG TTCAATAAAA	A	-1000193	M17886	Human acidic ribosomal phosphoprotein P1 mRNA, com
				J05068	human transcobalamin I mRNA, complete cds.
27	CATG CGACCCACG	C	-398663	M12529	Human apolipoprotein E mRNA, complete cds.
				K00396	Human apolipoprotein E (epsilon 2 and 3 alleles) m
28	CATG CAGATCTTTG	T	-298495	X56998	Human Uba52 adrenal mRNA for ubiquitin-52 amino ac
				X56999	Human Uba52 placental mRNA for ubiquitin-52 amino
29	CATG CTGGCGAGCG	C	-501287	X07491	Human DNA inserts showing sperm-specific hypomethy
				M91670	Human ubiquitin carrier protein (E2-EPE) mRNA, com
30	CATG ATGGCTTAA	A	-256497	L14272	Human prohibitin (PHB) gene, exons 1-7.
				S85655	prohibitin [human, mRNA, 1043 nt].
31	CATG GTGGTGGACA	C	-765573	U62435	Human nicotinic acetylcholine receptor alpha6 subu
				U68041	Human breast and ovarian cancer susceptibility pro
32	CATG TCCTGCCCCA	T	-883029	M24398	Human parathymosin mRNA, complete cds.
33	CATG ACTGGGTCTA	T	-125661	X58965	H. sapiens RNA for nm23-H2 gene.
				M36981	Human putative NDP kinase (nm23-H2S) mRNA, complet
				L16785	Human putative c-myc transcription factor (puf) mRNA
34	CATG AAGAAGATAG	A	-33331	U02032	Homo sapiens c-myc transcription factor (puf) mRNA
				U37230	Human ribosomal protein L23a mRNA, partial cds.
				U43701	Human ribosomal protein L23a mRNA, complete cds.
					Human ribosomal protein L23a mRNA, complete cds.

				L13799	Homo sapiens (clone 01) liver expressed protein mR
35	CATG ACATCATCGA	T	-79065	L06505	Human ribosomal protein L12 mRNA, complete cds.
36	CATG CTGTTGGTGA	T	-507577	D14530	Human homolog of yeast ribosomal protein S28, comp
37	CATG ATTATTTTTC	T	-249854	X57959	H.sapiens mRNA for ribosomal protein L7.
				X57958	H.sapiens mRNA for ribosomal protein L7.
				X52967	Human mRNA for ribosomal protein L7.
				L16558	Human ribosomal protein L7 (RPL7) mRNA, complete c
38	CATG GCITTTAAGG	A	-655115	L06498	Homo sapiens ribosomal protein S20 (RPS20) mRNA, c
39	CATG GGCAGARGA	A	-672265	L19527	Homo sapiens ribosomal protein L27 (RPL27) mRNA, c
				L25346	Homo sapiens ribosomal protein L27 (homologue of r
40	CATG CTCITCGAGA	A	-490889	Y00433	Homo sapiens ribosomal protein L27 (homologue of r
				Y00483	Human mRNA for glutathione peroxidase (EC 1.1.1.9
				X13710	Human gene for glutathione peroxidase.
				X13709	H.sapiens unspliced mRNA for glutathione peroxidase
				M21304	Human gpx1 mRNA for glutathione peroxidase.
				X04347	Human glutathione peroxidase (GPX1) mRNA, complete
41	CATG CTGTTGATTG	C	-507455	U00947	Human liver mRNA fragment DNA binding protein UPI
				M81757	Human clone C4E 3.2 (CAC)n/(GTG)n repeat-contains
42	CATG CTGGGTTAAT	A	-502724	X17206	Human S19 ribosomal protein mRNA, complete cds
43	CATG ATGGCTGGTA	T	-239533	X59357	H.sapiens mRNA for LLRep3.
44	CATG GATGCTGCCA	A	-583573	L21756	Human mRNA for Epstein-Barr virus small RNAs (EBER
				D17652	Human mRNA for acute myeloid leukemia associated pro
				S76343	Homo sapiens acute myeloid leukemia associated pro
				U14970	Human mRNA for HBp15/L22, complete cds.
45	CATG CCTTCGAGAT	C	-390692	U16811	Human mRNA for translocation breakpoint) [human, chro
46	CATG CTCCTCACCT	G	-482584	U23765	AML1...EAP (translocation breakpoint) [human, chro
				X16869	Human ribosomal protein S5 mRNA, complete cds.
47	CATG TGTGTTGAGA	G	-978825	X16872	Human Bak protein mRNA, complete cds.
				X03558	Human Bak protein mRNA, complete cds.
				D17182	Human mRNA for elongation factor 1-alpha (clone CE
				D17245	Human DNA for elongation factor 1-alpha (clone lam
				D17259	Human mRNA for elongation factor 1 alpha subunit (
				D17276	Human HepG2 3' region MboI cDNA, clone hmd2h03m3.
					Human HepG2 3' region MboI cDNA, clone hmd4h05m3.
					Human HepG2 3' region MboI cDNA, clone hmd5d07m3.
					Human HepG2 3' region MboI cDNA, clone hmd6a12m3.

			M27364	Human elongation factor 1 alpha mRNA, 3' end.
			M29548	Human e'ngation factor 1-alpha (EF1A) mRNA, parti
			I41490	Homo sapiens oncogene PTI-1 mRNA, complete cds.
			I41498	Homo sapiens oncogene PTI-1 mRNA, complete cds.
				Human ribosomal protein L39 mRNA, complete cds.
48	CATG TTACCATATC	A	-988366 U57846	H. sapiens GPx-4 mRNA for phospholipid hydroperoxid
49	CATG GCCTGCTGGG	C	-621035 X71973	H. sapiens gene for ribosomal protein L38.
50	CATG CCTCGGAAAA	T	-383489 Z26876	H. sapiens mRNA for ribosomal protein L6.
51	CATG TACAGAGGGA	A	-803369 X69391	Human mRNA for DNA-binding protein, TAXREB107, com
			-803369 D17554	neoplasm-related C140 product [human, thyroid carc
			-803369 S71022	Human beta-tubulin pseudogene.
52	CATG AACGACCTCG	T	-24951 V00598	Human mRNA fragment encoding beta-tubulin. (from c
			-24951 V00599	Human mRNA for neurite outgrowth-promoting protein
53	CATG CCCTGCCTTG	T	-358783 X55110	Human stimulator of TAR RNA binding (SRB) mRNA, co
54	CATG CCCAGGGAGA	A	-346761 U38846	Human HepG2 3' region cDNA, clone hmd4f11.
			D16933	H. sapiens mRNA for elongation factor 2.
55	CATG AGCACCTCCA	G	-148949 Z11692	H. sapiens HRPL4 mRNA.
56	CATG CGCCGGAACA	C	-416261 X73974	Human mRNA for ribosomal protein, complete cds.
			D23660	Human 26-kDa cell surface protein TAPA-1 mRNA, com
57	CATG CTAATAAAAA	A	-458753 M33680	Human glycyl-tRNA synthetase mRNA, complete cds.
58	CATG GGCTGATGTG	G	-686319 U09510	Human glycyl-tRNA synthetase mRNA, complete cds.
			U09587	Human T-cell mRNA for glycyl tRNA synthetase, comp
			D30658	Human mRNA for HL23 ribosomal protein homologue.
59	CATG ATTCTCCAGT	A	-253260 X55954	Human mRNA for ribosomal protein L17.
			X52839	H. sapiens mRNA for laminin-binding protein.
60	CATG GAAAATGGT	T	-524524 X61156	Human mRNA for potential laminin-binding protein (
			X15005	Human 37 kD laminin receptor precursor/p40 ribosom
			U43901	Human colon carcinoma laminin-binding protein mRNA
			J03799	Human laminin receptor (2H5 epitope) mRNA, 5' end.
			M14199	Human mRNA for ribosomal protein L14, complete cds
61	CATG CAGCTCACTG	A	-302367 D87735	Human (clone CTG-B33) mRNA sequence.
			L10376	CAG-isl 7 [trinucleotide repeat-containing sequenc
			S80520	Human ribosomal protein S29 mRNA, complete cds.
62	CATG ATAATTCTTT	G	-200576 U14973	

			L31610	Homo sapiens (clone cori-lc15) S29 ribosomal prote
63	CATG AATCTGTGG	A	-55227	H.sapiens mRNA for ribosomal protein L8.
64	CATG AATAGGTCCA	A	-51925	Human ribosomal protein S25 mRNA, complete cds.
65	CATG AAAAAAAAAA	A (C, G,T)	-1	H.sapiens B1 mRNA for mucin.
			X83412	H.sapiens FRGAMMA mRNA (819bp) for folate receptor
			Z32564	H.sapiens FRGAMMA' mRNA for folate receptor (817bp
			Z32633	H.sapiens FRGAMMA' mRNA for folate receptor (817bp
			X76180	H.sapiens mRNA for lung amiloride sensitive Na+ ch
			U08470	Human FR-gamma' mRNA, complete cds.
			U08471	Human folate receptor 3 mRNA, complete cds.
			U48697	Human mariner-like element-containing mRNA, clone
			D28532	Human mRNA for renal Na+-dependent phosphate cotra
			M55914	Human c-myc binding protein (MBP-1) mRNA, complete
			L06175	Homo Sapiens P5-1 mRNA, complete cds.
			S73775	calmitine-mitochondrial calcium-binding protein [h
			S77393	transcript chl38 [human, RFL, RF48 stomach cancer c
			X60036	H.sapiens mRNA for mitochondrial phosphate carrier
			X79238	H.sapiens mRNA for ribosomal protein L30.
66	CATG CCAGAACAGA	C	-335945	H.sapiens mRNA for ribosomal protein L30.
			L16991	Human thymidylate kinase (CDC8) mRNA, complete cds
			X80822	H.sapiens mRNA for ORF.
67	CATG AAGGTGGAGG	A	-44683	Human cyclophilin-related processed pseudogene.
68	CATG CCTAGCTGGA	T	-379369	Human cyclophilin-related processed pseudogene.
			X52857	Human cyclophilin-related processed pseudogene.
			X52854	Human cyclophilin-related processed pseudogene.
			X52851	Human cyclophilin gene for cyclophilin (EC 5.2.1.8
			Y00052	Human mRNA for T-cell cyclophilin.
			X63527	H.sapiens mRNA for ribosomal protein L19.
69	CATG GAACACATCC	A	-528694	ribosomal protein L19 [human, breast cancer cell 1
			S56985	H.sapiens mRNA for ribosomal protein L31.
70	CATG AAGGAGATGG	G	-41531	Human mRNA for ribosomal protein L31.
			X15940	H.sapiens SMCX mRNA.
71	CATG AGGCTACGGA	A	-171113	Human Hep2 3' region MboI cDNA, clone hmd4cl2m3.
			D17233	Human GST pi gene for glutathione S-transferase pi
72	CATG AGGCTCTAGC	C	-177610	

		X06547	Human mRNA for class PI glutathione S-transferase
		X15480	Human mRNA for anionic glutathione S-transferase (
		X08058	Human glutathione S-transferase pi gene.
		U12472	Human glutathione S-transferase (GST phi) gene, co
		U21689	Human glutathione S-transferase-Plc gene, complete
		U62589	Human glutathione S-transferase Plc (GSTplc) mRNA,
		M69113	Human fatty acid ethyl ester synthase-III mRNA seq
		M24485	Homo sapiens (clone pGST-pi) glutathione S-transf
		-965603	H.sapiens mRNA for ribosomal protein S18.
73	CATG TGGTGTGAG G	X69150	Homo sapiens apolipoprotein B gene sequence.
		M96153	Homo sapiens 18S ribosomal protein (HKE3) mRNA seq
		L06432	Homo sapiens 18S ribosomal phosphoprotein P0 mRNA, com
		M17885	Human acidic ribosomal phosphoprotein L10 mRNA, complete cds.
74	CATG CTCACATCT C	-475448	Human ribosomal protein L10 mRNA, complete cds.
75	CATG GTGTTAACCA G	-769045	Human (D9S55) DNA segment containing (TG)24 repeat
76	CATG AGGCTTCCA A	-174037	Human HepG2 3' region MboI cDNA, clone hmd5h09m3.
		D17268	Human novel gene mRNA, complete cds.
		M73791	Human Wilms' tumor-related protein (QM) mRNA, comp
		M64241	laminin receptor homolog (3' region) [human, mRNA
		S35960	Human acidic ribosomal phosphoprotein P2 mRNA, com
		-671654	Human ferritin L chain mRNA, complete cds.
77	CATG GGATTGGCC T	M11147	Human ferritin light subunit mRNA, partial cds.
		M12938	Human ferritin light subunit mRNA, complete cds.
		M10119	Human mRNA for coupling protein G(s) alpha-subunit
78	CATG ATTACCAAG C	-246019	Human mRNA for coupling protein G(s) alpha subunit
		X04408	Human GSA mRNA for alpha subunit of GsGTP binding
		X56009	Human mRNA stimulatory GTP-binding protein alpha s
		X07036	Human guanine nucleotide-binding protein alpha-sub
		M21142	Human guanine nucleotide-binding protein G-s, alph
		M14631	H.sapiens (xs31) mRNA, 835bp.
79	CATG TGTACCTGTA A	-968173	human alpha-tubulin mRNA, complete cds.
		K00558	H.sapiens M gene for M1-type and M2-type pyruvate
80	CATG TGCCCCCACC C	-955718	Human M2-type pyruvate kinase mRNA, complete cds.
		M23725	Human TCB gene encoding cytosolic thyroid hormone-
		M26252	

81	CATG TAATRAAGGT	G	-798764	X67247	H.sapiens rps8 gene for ribosomal protein S8.
82	CATG GCATAATAGG	T	-602315	X89401	H.sapiens mRNA for large subunit of ribosomal prot
				U14967	Human ribosomal protein L21 mRNA, complete cds.
				U25789	Human ribosomal protein L21 mRNA, complete cds.
				L38826	Homo sapiens L21 ribosomal protein gene, partial c
83	CATG TACCATCAAT	A	-807748	X53778	H.sapiens hng mRNA for uracil DNA glycosylase.
				U34995	Human normal keratinocyte subtraction library mRN
				J02642	Human glyceraldehyde 3-phosphate dehydrogenase mRN
				M36164	Human glyceraldehyde 3-phosphate dehydrogenase mRN
				M33197	Human glyceraldehyde 3-phosphate dehydrogenase (GA
94	CATG ATTTGTCCCA	G	-260949	X14957	Human hmgI mRNA for high mobility group protein I.
				X14958	Human hmgI mRNA for high mobility group protein Y.
				M23614	Human HMG-I protein isoform mRNA (HMG1 gene), clon
				M23619	Human HMG-I protein isoform mRNA (HMG1 gene), clon
				L17131	Human high mobility group protein (HMG-I(Y)) gene
				M23615	Human HMG-Y protein isoform mRNA (HMG1 gene), clon
				M23616	Human HMG-Y protein isoform mRNA (HMG1 gene), clon
				M23617	Human HMG-Y protein isoform mRNA (HMG1 gene), clon
				M23618	Human HMG-Y protein isoform mRNA (HMG1 gene), clon
95	CATG GAGGAGTTT	C	-567488	U14968	Human ribosomal protein L27a mRNA, complete cds.
86	CATG CGCGCGCGC	T	-416106	U12465	Human ribosomal protein L35 mRNA, complete cds.
87	CATG GTGAAACCCA	ALL	-753749	Z63072	H.sapiens CpG island DNA genomic MseI fragment, cl
88	CATG GTGAAACCCA	ALL	-753749	X16294	Human repetitive DNA containing interspersed repea
89	CATG AAGACAGTGG	C	-33979	X66699	H.sapiens mRNA for ribosomal protein L37a.
				L06499	Homo sapiens ribosomal protein L37a (RPL37A) mRNA,
				L22154	Human ribosomal protein L37a mRNA sequence.
90	CATG CCCAGCCAG	T	-348755	X55715	Human Hums3 mRNA for 40S ribosomal protein s3.
				U14990	Human XP1PO ribosomal protein S3 (rps3) mRNA, comp
				U14991	Human XP2NE ribosomal protein S3 (rps3) mRNA, comp
				U14992	Human IMR-90 ribosomal protein S3 (rps3) mRNA, com
				S42658	S3 ribosomal protein [human, colon, mRNA, 826 nt].
91	CATG TGGGCAAGC	C	-959498	X63526	H.sapiens mRNA for protein homologous to elongatio
				Z11531	H.sapiens mRNA for elongation factor-I-gamma.

			M55409	Human pancreatic tumor-related protein mRNA, 3' en
92	CATG TGAGGGAATA A	-928269	M10036	Human triosephosphate isomerase mRNA, complete cds
93	CATG GACGACACGA G	-549145	U58682	Human ribosomal protein S28 mRNA, complete cds.
			M58458	Human ribosomal protein S4 (RPS4X) isoform mRNA, c
			M22146	Human scar protein mRNA, complete cds.
94	CATG AACGGGGCCA A	-26261	Z23063	Homo sapiens macrophage migration inhibitory facto
			L10612	Human glycosylation-inhibiting factor mRNA, comple
			M95775	Homo sapiens macrophage migration inhibitory facto
			L19686	Homo sapiens macrophage migration inhibitory facto
			M25639	Human migration inhibitory factor (MIF) mRNA, comp
95	CATG TGCACGTTT C	-935680	X03342	Human mRNA for ribosomal protein L32.
			K03002	Human mRNA from chromosome 15 gene with homology t
96	CATG CACAAACGGT A	-278636	U57847	Human ribosomal protein S27 mRNA, complete cds.
			L19739	Homo sapiens metalloproteinin (MPS1) mRNA, compl
97	CATG GGAGTGACA T	-667269	L11566	Homo sapiens ribosomal protein L18 (RPL18) mRNA, c
98	CATG GCCGAGAAG G	-615043	Z54999	H.sapiens CpG island DNA genomic MseI fragment, cl
			Z57572	H.sapiens CpG island DNA genomic MseI fragment, cl
			Z56073	H.sapiens CpG island DNA genomic MseI fragment, cl
			X53505	Human mRNA for ribosomal protein S12.
99	CATG GGGGAAATCG C	-696375	M92381	Human thymosin beta 10 mRNA, complete cds.
			M20259	Human thymosin beta-10 mRNA, complete cds.
100	CATG GCAGCCATCC G	-599350	U14969	Human ribosomal protein L28 mRNA, complete cds.
			D17257	Human HepG2 3' region MboI cDNA, clone hmd5d04m3.
101	CATG TAAGGAGCTG A	-796831	X77770	H.sapiens RPS26 mRNA.
			X69654	H.sapiens mRNA for ribosomal protein S26.
102	CATG GGCAAGCCCC A	-672342	U12404	Human Csa-19 mRNA, complete cds.
			X79239	H.sapiens mRNA for ribosomal protein S13.
			L01124	Human ribosomal protein S13 (RPS13) mRNA, complete
103	CATG GTTCCTGGC C	-775658	X65923	H.sapiens fau mRNA.
			U02523	Human FAU1P pseudogene, trinucleotide repeat regio
104	CATG CCGTCAAGG G	-374027	M60854	Human ribosomal protein S16 mRNA, complete cds.
	CATG TTGGTCTCT G	-1027448	Z12962	H.sapiens mRNA for homologue to yeast ribosomal pr
			S64030	L41 ribosomal protein homolog (clone 7B6) [human,

105	CATG CAAACCATCC	A	-263478	X12883	Human mRNA for cytokeratin 18.
				X12876	Human mRNA fragment for cytokeratin 18.
				X12881	Human mRNA for cytokeratin 18.
				M24842	Human keratin 18 (K18) gene, complete cds.
				M26325	Human cytokeratin 18 mRNA, 3' end.
				M26326	Human keratin 18 mRNA, complete cds.
				M26327	Human cytokeratin 18 mRNA, 3' end.
				X53777	Human L23 mRNA for putative ribosomal protein.
106	CATG AGCTCTCCCT	G	-161624	D86979	Human male bone marrow myeloblast mRNA for KIAA022
107	CATG AGGTCAGGAG	A(T)	-177315	X55923	Human DNA for Alu element pIN6.
				X79699	H. sapiens ALU repeat, 230bp.
				X12544	Human mRNA for HLA class II DR-beta (HLA-DR B).
				Z77989	H. sapiens flow-sorted chromosome 6 HindIII fragmen
				U11831	Human clone 2102V-1 chromosome 18p telomeric seque
				U12580	Human Alu repeat sequence A3.
				U12582	Human Alu repeat sequence B2.
				U12583	Human Alu repeat sequence D1.
				U14694	Human Alu-Sb2 repeat, clone HALUSB08.
				U14695	Human Alu-Sb2 repeat, clone HALUSB15.
				U14696	Human Alu-Sb2 repeat, clone HALUSB27.
				U14697	Human Alu-Sb2 repeat, clone HUM-11.
				U14698	Human Alu-Sb2 repeat, clone HSB-8P.
				U14699	Human Alu-Sb2 repeat, clone HUM-9.
				U14700	Human Alu-Sb2 repeat, clone HALUSB35.
				U14701	Human Alu-Sb2 repeat, clone HSB-2P.
				U14704	Human Alu-Sb2 repeat, clone HUM-3.
				U14706	Human Alu-Sb2 repeat, clone HUM-10.
				U14707	Human Alu-Sb2 repeat, clone HUM-7.
				J00120	Human (Lawn) c-myc proto-oncogene, complete coding
				L34653	Homo sapiens platelet/endothelial cell adhesion mo
				M37521	Human XV2c gene.
				S61789	NF1-neurofibromatosis type 1 (deletion breakpoint,
				S73483	phosphorylase kinase catalytic subunit PHKG2 homol

			S75201	cholinesterase (Alu element) [human, Insertion Mut
			S75337	[Y Alu polymorphism, YAP, polymorphic subfamily-3)
108	CATG GGCTGGGT C	-695980	Z49148	H. sapiens mRNA for ribosomal protein L29.
			U10248	Human ribosomal protein L29 (humrpl29) mRNA, compl
			U49083	Human cell surface heparin binding protein HIP mRNA
			D16992	Human HepG2 partial cDNA, clone hmd2d02m5.
			D16911	Human HepG2 3' region cDNA, clone hmd3b09.
			J03537	Human ribosomal protein S6 mRNA, complete cds.
			M20020	Human ribosomal protein S6 mRNA, complete cds.
				EST
109	CATG ACGTCTCTT C	-114144		EST
110	CATG TCTCATACC C	-906438		EST
111	CATG GACTGCGTC C	-555450		EST
112	CATG CTTATCCTG A	-508767		EST
113	CATG GGTGGCAGG G	-719435		EST
114	CATG GCCCTCTGCC A	-613862		EST
115	CATG AACAGAAGCA A	-18469		EST
116	CATG CTGCCGAGCT C	-497192		EST
117	CATG TTCCTCGGC A	-1007018		EST
118	CATG AACTAATACT A	-28872		EST
119	CATG TAGATAATGG C	-822331		EST
120	CATG GCCACACCC A,C	-607318		EST
121	CATG GAACCTGGG A	-529899		EST
122	CATG AACTAAAAA A	-28673		EST
123	CATG GAATGTAG A	-528067		EST
124	CATG ACTCAAAA A	-119809		EST
125	CATG GTTCGTGCC A	-777109		EST
126	CATG TTACCTCCTT C	-989024		EST
127	CATG GCACAGAG A	-594051		EST
128	CATG CCCTGGGTC T	-359102		EST
129	CATG GCCTGTATGA G	-621369		EST
130	CATG CCGTCCGGA A	-355689		EST
131	CATG AGGAAGCTG C	-163999		EST
132	CATG TCAGATCTTT G	-861056		EST

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133	CATG	CCAGGAGGAA	T	-338081
134	CATG	TCACCCACAC	C	-857362
135	CATG	GTGTTGCACA	A	-769605
136	CATG	GCCGTGTCCG	C	-618199

Isolation of partial cDNA (3' fragment) by 3' directed PCR reaction

This procedure is a modification of the protocol described in Polyak et al. (1997) Nature 389:300. Briefly, the procedure uses SAGE tags in PCR reaction such that the resultant PCR product contains the SAGE tag of interest as well as additional cDNA, the length of which is defined by the position of the tag with respect to the 3' end of the cDNA. The cDNA product derived from such a transcript driven PCR reaction can be used for many applications.

RNA from a source believed to express the cDNA corresponding to a given tag is first converted to double-stranded cDNA using any standard cDNA protocol. Similar conditions used to generate cDNA for SAGE library construction can be employed except that a modified oligo-dT primer is used to drive the first strand synthesis. For example, the oligonucleotide of composition 5'-B-TCC GGC GCG CCG TTT T CC CAG TCA CGA(30)-3', contains a poly-T stretch at the 3' end for hybridization and priming from poly-A tails, an M13 priming site for use in subsequent PCR steps, a 5' Biotin label (B) for capture to streptavidin-coated magnetic beads, and an *AscI* restriction endonuclease site for releasing the cDNA from the streptavidin-coated magnetic beads. Theoretically, any sufficiently-sized DNA region capable of hybridizing to a PCR primer can be used as well as any other 8 base pair recognizing endonuclease.

cDNA constructed utilizing this or similar modified oligo-dT primer is then processed exactly as described in U.S. Patent No. (insert) up until adapter ligation where only one adapter is ligated to the cDNA pool. After adapter ligation, the cDNA is released from the streptavidin-coated magnetic beads and is then used as a template for cDNA amplification.

Various PCR protocols can be employed using PCR priming sites within the 3' modified oligo-dT primer and the SAGE tag. The SAGE tag-derived PCR primer employed can be of varying length dictated by 5' extension of the tag into the adaptor sequence. cDNA products are now available for a variety of applications.

This technique can be further modified by: (1) altering the length and/or content of the modified oligo-dT primer; (2) ligating adaptors other than that previously employed within the SAGE protocol; (3) performing PCR from template retained on the streptavidin-coated magnetic beads; and (4) priming first strand cDNA synthesis with non-oligo-dT based primers.

Isolation of cDNA using GeneTrapper or modified GeneTrapper Technology

The reagents and manufacturer's instructions for this technology are commercially available from Life Technologies, Inc., Gaithersburg, Maryland. Briefly, a complex population of single-stranded phagemid DNA containing directional cDNA inserts is enriched for the target sequence by hybridization in solution to a biotinylated oligonucleotide probe complementary to the target sequence. The hybrids are captured on streptavidin-coated paramagnetic beads. A magnet retrieves the paramagnetic beads from the solution, leaving nonhybridized single-stranded DNAs behind. Subsequently, the captured single-stranded DNA target is released from the biotinylated oligonucleotide. After release, the cDNA clone is further enriched by using a nonbiotinylated target oligonucleotide to specifically prime conversion of the single-stranded target to double-stranded DNA. Following transformation and plating, typically 20% to 100% of the colonies represent the cDNA clone of interest. To identify the desired cDNA clone, the colonies may be screened by colony hybridization using the ³²P-labeled oligonucleotide as described above for solution hybridization, or alternatively by DNA sequencing and alignment of all sequences obtained from numerous clones to determine a consensus sequence.

The genes which are identified herein as being differentially expressed in normal and cancer cells can be used diagnostically and prognostically. Transcription levels in a test sample suspected of being neoplastic can be determined and compared to the levels in normal colon cells. The test sample may be from any tissue suspected of neoplasia, and particularly from either suspected colorectal or suspected pancreatic cancer cells. The control cells for

the purposes of comparison are normal cells, preferably of the same tissue type as the test sample, *e.g.*, colon cells, or pancreatic duct epithelial cells. Upregulation of transcription or downregulation of transcription is therefore diagnostic of the neoplastic state, depending on what gene is used as a test reagent. Similarly, transcription levels can be monitored to assess patient responses to anti-tumor therapies. Transcription levels will also provide prognostic information. For example, the level of transcription in a test sample can be compared to levels found in *bona fide* normal and tumor cells. More extreme deviations from normal expression levels indicate a poorer prognosis.

Transcription levels can be determined according to any means known in the art. These include, without limitation, Northern blots, nuclear run-on assays, *in vitro* transcription assays, primer extension assays, quantitative reverse transcriptase-polymerase chain reactions (RT-PCR), and hybrid filter binding assays. These techniques are well known in the art. See J.C. Alwine, D.J. Kemp, G.R. Stark, *Proc. Natl. Acad. Sci. U.S.A.* 74, 5350 (1977); K. Zinn, D. Di-Maio, T. Maniatis, *Cell* 34, 865 (1983); G. Veres, R.A. Gibbs, S.E. Scherer, C.T. Caskey, *Science* 237, 415 (1987).

Similarly, upregulated genes and downregulated genes can be detected by measuring expression of their protein products. This can be done by any means known in the art, including but not limited to Western (immuno) blot, enzyme linked immunoadsorbent assay, radioimmunoassay, and enzyme assay. Such techniques are well known in the art. Protein products can be detected in tissue samples of a test patient, using a suspect sample as a test sample, and a matched normal tissue sample from the same tissue type as a control. If normal tissue is not available then a closely related tissue type can be used. Desirably both the samples being compared will be from the same individual. Alternatively, aberrant expression levels of protein products can be detected in body samples, such as blood, serum, feces, urine, sputum. As a control, a normal matched sample can be used from a healthy individual. Aberrant expression levels of transcripts can also be detected in such body samples, particularly in blood and serum.

Probes for use in the assays for transcription levels of particular genes or sets of genes may be RNA or DNA. The probes will be isolated substantially free of other cellular RNAs or DNAs. If the reagent contains one probe then it will comprise at least 50% of the nucleic acids in the reagent composition. If the reagent contains more than one probe, then the proportion will decrease accordingly, so that specific probes will still comprise at least 50% of the nucleic acids in the reagent composition.

Probes can be labeled according to any means known in the art. These may include radioactive labels, fluorescent labels, enzymatic labels, and binding partner labels such as biotin. Means for labeling and detecting probes are well known in the art. Probes comprise at least 10, 11, 12, 15, 20, or 30 contiguous nucleotides of a selected gene.

This invention provides proteins or polypeptides expressed from the polynucleotides of this invention, which is intended to include wild-type and recombinantly produced polypeptides and proteins from procaryotic and eucaryotic host cells, as well as muteins, analogs and fragments thereof. In some embodiments, the term also includes antibodies and anti-idiotypic antibodies.

It is understood that functional equivalents or variants of the wild-type polypeptide or protein also are within the scope of this invention, for example, those having conservative amino acid substitutions. Other analogs include fusion proteins comprising a protein or polypeptide.

The proteins and polypeptides of this invention are obtainable by a number of processes well known to those of skill in the art, which include purification, chemical synthesis and recombinant methods. Full length proteins can be purified from a colon or pancreatic cell or tissue lysate by methods such as immunoprecipitation with antibody, and standard techniques such as gel filtration, ion-exchange, reversed-phase, and affinity chromatography using a fusion protein as shown herein. For such methodology, see for example Deutscher et al. (1999) Guide To Protein Purification: Methods In Enzymology (Vol. 182, Academic Press). Accordingly, this invention also

provides the processes for obtaining these proteins and polypeptides as well as the products obtainable and obtained by these processes.

5 The proteins and polypeptides also can be obtained by chemical synthesis using a commercially available automated peptide synthesizer such as those manufactured by Perkin Elmer/Applied Biosystems, Inc., Model 430A or 431A, Foster City. The synthesized protein or polypeptide can be precipitated and further purified, for example by high performance liquid chromatography (HPLC). Accordingly, this invention also provides a process for chemically synthesizing the proteins of this invention by providing the
10 sequence of the protein and reagents, such as amino acids and enzymes and linking together the amino acids in the proper orientation and linear sequence.

Alternatively, the proteins and polypeptides can be obtained by well-known recombinant methods as described, for example, in Sambrook et al., (1989), supra, using the host cell and vector systems described above.

15 Also provided by this application are the polypeptides and proteins described herein conjugated to a detectable agent for use in the diagnostic methods. For example, detectably labeled proteins and polypeptides can be bound to a column and used for the detection and purification of antibodies. They also are useful as immunogens for the production of antibodies as
20 described below. The proteins and fragments of this invention are useful in an in vitro assay system to screen for agents or drugs, which modulate cellular processes.

The proteins of this invention also can be combined with various liquid phase carriers, such as sterile or aqueous solutions, pharmaceutically
25 acceptable carriers, suspensions and emulsions. Examples of non-aqueous solvents include propyl ethylene glycol, polyethylene glycol and vegetable oils. When used to prepare antibodies, the carriers also can include an adjuvant that is useful to non-specifically augment a specific immune response. A skilled artisan can easily determine whether an adjuvant is required and select one.
30 However, for the purpose of illustration only, suitable adjuvants include, but

are not limited to Freund's Complete and Incomplete, mineral salts and polynucleotides.

This invention also provides a pharmaceutical composition comprising any of a protein, analog, mutein, polypeptide fragment, antibody, antibody
5 fragment or anti-idiotypic antibody of this invention, alone or in combination with each other or other agents, and an acceptable carrier. These compositions are useful for various diagnostic and therapeutic methods.

Antibodies can be generated using the proteins encoded by the transcripts identified by the tags disclosed herein. Use of all or portions of the
10 protein as immunogens is routine in the art. Similarly, fusion proteins can be used as immunogens. Antibodies can be affinity purified using the proteins or portions thereof used as immunogens. Similarly, monoclonal antibodies specifically immunoreactive with the protein sequences of the invention can be generated according to techniques which are well known in the art.

Antibodies can be used analytically to quantitate the expression of
15 particular transcripts identified herein as upregulated or downregulated in cancer. In addition, antibodies can be conjugated or non-covalently linked to cytotoxic agents, such as cytotoxins, radionuclides, chemotherapeutic drugs, etc. Such antibodies can be used therapeutically to specifically target cancer
20 cells in which the protein antigens are upregulated. These include the proteins encoded by the transcripts identified by the tags shown in Tables 2, 4, and 5. Means of making such linked cytotoxic antibodies and of administering the same are well known in the art.

Also provided by this invention is an antibody capable of specifically
25 forming a complex with the proteins or polypeptides as described above. The term "antibody" includes polyclonal antibodies and monoclonal antibodies. The antibodies include, but are not limited to mouse, rat, and rabbit or human antibodies.

Laboratory methods for producing polyclonal antibodies and
30 monoclonal antibodies, as well as deducing their corresponding nucleic acid sequences, are known in the art, see Harlow and Lane (1988) supra and

Sambrook et al. (1989) supra. The monoclonal antibodies of this invention can be biologically produced by introducing protein or a fragment thereof into an animal, e.g., a mouse or a rabbit. The antibody producing cells in the animal are isolated and fused with myeloma cells or heteromyeloma cells to produce hybrid cells or hybridomas. Accordingly, the hybridoma cells producing the monoclonal antibodies of this invention also are provided.

Thus, using the protein or fragment thereof, and well known methods, one of skill in the art can produce and screen the hybridoma cells and antibodies of this invention for antibodies having the ability to bind the proteins or polypeptides.

If a monoclonal antibody being tested binds with the protein or polypeptide, then the antibody being tested and the antibodies provided by the hybridomas of this invention are equivalent. It also is possible to determine without undue experimentation, whether an antibody has the same specificity as the monoclonal antibody of this invention by determining whether the antibody being tested prevents a monoclonal antibody of this invention from binding the protein or polypeptide with which the monoclonal antibody is normally reactive. If the antibody being tested competes with the monoclonal antibody of the invention as shown by a decrease in binding by the monoclonal antibody of this invention, then it is likely that the two antibodies bind to the same or a closely related epitope. Alternatively, one can pre-incubate the monoclonal antibody of this invention with a protein with which it is normally reactive, and determine if the monoclonal antibody being tested is inhibited in its ability to bind the antigen. If the monoclonal antibody being tested is inhibited then, in all likelihood, it has the same, or a closely related, epitopic specificity as the monoclonal antibody of this invention.

The term "antibody" also is intended to include antibodies of all isotypes. Particular isotypes of a monoclonal antibody can be prepared either directly by selecting from the initial fusion, or prepared secondarily, from a parental hybridoma secreting a monoclonal antibody of different isotype by using the sib selection technique to isolate class switch variants using the

procedure described in Steplewski et al. (1985) Proc. Natl. Acad. Sci. 82:8653 or Spira et al. (1984) J. Immunol. Methods 74:307.

This invention also provides biological active fragments of the polyclonal and monoclonal antibodies described above. These "antibody fragments" retain some ability to selectively bind with its antigen or immunogen. Such antibody fragments can include, but are not limited to:

- (1) Fab,
- (2) Fab',
- (3) F(ab')₂,
- (4) Fv, and
- (5) SCA

A specific example of "a biologically active antibody fragment" is a CDR region of the antibody. Methods of making these fragments are known in the art, see for example, Harlow and Lane, (1988) supra.

The antibodies of this invention also can be modified to create chimeric antibodies and humanized antibodies (Oi, et al. (1986) BioTechniques 4(3):214). Chimeric antibodies are those in which the various domains of the antibodies' heavy and light chains are coded for by DNA from more than one species.

The isolation of other hybridomas secreting monoclonal antibodies with the specificity of the monoclonal antibodies of the invention can also be accomplished by one of ordinary skill in the art by producing anti-idiotypic antibodies (Herlyn, et al. (1986) Science 232:100). An anti-idiotypic antibody is an antibody which recognizes unique determinants present on the monoclonal antibody produced by the hybridoma of interest.

Idiotypic identity between monoclonal antibodies of two hybridomas demonstrates that the two monoclonal antibodies are the same with respect to their recognition of the same epitopic determinant. Thus, by using antibodies to the epitopic determinants on a monoclonal antibody it is possible to identify other hybridomas expressing monoclonal antibodies of the same epitopic specificity.

It is also possible to use the anti-idiotypic technology to produce monoclonal antibodies which mimic an epitope. For example, an anti-idiotypic monoclonal antibody made to a first monoclonal antibody will have a binding domain in the hypervariable region which is the mirror image of the epitope bound by the first monoclonal antibody. Thus, in this instance, the anti-idiotypic monoclonal antibody could be used for immunization for production of these antibodies.

As used in this invention, the term "epitope" is meant to include any determinant having specific affinity for the monoclonal antibodies of the invention. Epitopic determinants usually consist of chemically active surface groupings of molecules such as amino acids or sugar side chains and usually have specific three dimensional structural characteristics, as well as specific charge characteristics.

The antibodies of this invention can be linked to a detectable agent or label. There are many different labels and methods of labeling known to those of ordinary skill in the art.

The antibody-label complex is useful to detect the protein or fragments in a sample, using standard immunochemical techniques such as immunohistochemistry as described by Harlow and Lane (1988) *supra*. Competitive and non-competitive immunoassays in either a direct or indirect format are examples of such assays, e.g., enzyme linked immunoassay (ELISA) radioimmunoassay (RIA) and the sandwich (immunometric) assay. Those of skill in the art will know, or can readily discern, other immunoassay formats without undue experimentation.

The coupling of antibodies to low molecular weight haptens can increase the sensitivity of the assay. The haptens can then be specifically detected by means of a second reaction. For example, it is common to use haptens such as biotin, which reacts avidin, or dinitropherry, pyridoxal, and fluorescein, which can react with specific anti-hapten antibodies. See Harlow and Lane (1988) *supra*.

The monoclonal antibodies of the invention also can be bound to many different carriers. Thus, this invention also provides compositions containing the antibodies and another substance, active or inert. Examples of well-known carriers include glass, polystyrene, polypropylene, polyethylene, dextran, nylon, amylases, natural and modified celluloses, polyacrylamides, agaroses and magnetite. The nature of the carrier can be either soluble or insoluble for purposes of the invention. Those skilled in the art will know of other suitable carriers for binding monoclonal antibodies, or will be able to ascertain such, using routine experimentation.

Compositions containing the antibodies, fragments thereof or cell lines which produce the antibodies, are encompassed by this invention. When these compositions are to be used pharmaceutically, they are combined with a pharmaceutically acceptable carrier.

The present invention also provides a screen for various agents which modulate the expression of a gene in a pancreatic or colon cell. To practice the method in vitro, suitable cell cultures or tissue cultures are first provided. The cell can be a cultured cell or a genetically modified cell in which a transcript from SEQ ID NOS:1-732, or their complements, is expressed. Alternatively, the cells can be from a tissue biopsy. The cells are cultured under conditions (temperature, growth or culture medium and gas (CO₂)) and for an appropriate amount of time to attain exponential proliferation without density dependent constraints. It also is desirable to maintain an additional separate cell culture; one which does not receive the agent being tested as a control.

As is apparent to one of skill in the art, suitable cells may be cultured in microtiter plates and several agents may be assayed at the same time by noting genotypic changes, phenotypic changes or cell death.

When the agent is a composition other than a DNA or RNA, the agent may be directly added to the cell culture or added to culture medium for addition. As is apparent to those skilled in the art, an "effective" amount must be added which can be empirically determined. When the agent is a polynucleotide, it may be directly added by use of a gene gun or

electroporation. Alternatively, it may be inserted into the cell using a gene delivery vehicle or vector as described above.

5 An agent is a potential therapeutic if it alters the expression of gene in the cell. Altered expression can be detected by assaying for altered mRNA expression or protein expression using the probes, primers and antibodies as described herein.

10 For the purposes of this invention, an "agent" is intended to include, but not be limited to a biological or chemical compound such as a simple or complex organic or inorganic molecule, a peptide, a protein (e.g. antibody) or a polynucleotide (e.g. anti-sense). A vast array of compounds can be synthesized, for example polymers, such as polypeptides and polynucleotides, and synthetic organic compounds based on various core structures, and these are also included in the term "agent". In addition, various natural sources can provide compounds for screening, such as plant or animal extracts, and the like. It should be understood, although not always explicitly stated that the agent is used alone or in combination with another agent, having the same or different biological activity as the agents identified by the inventive screen. The agents and methods also are intended to be combined with other therapies.

20 The above disclosure generally describes the present invention. A more complete understanding can be obtained by reference to the following specific examples which are provided herein for purposes of illustration only, and are not intended to limit the scope of the invention.

EXAMPLE 1

25 This example demonstrates the characterization of the general transcription of human colorectal epithelium, colorectal cancers, and pancreatic cancers.

30 We used the recently developed SAGE (serial analysis of gene expression) method to identify and quantify a total of 303,706 transcripts derived from human colorectal (CR) epithelium, CR cancers or pancreatic cancers (Table 1A) (3). These transcripts represented approximately 48,741

different genes (4) that ranged in average expression from 1 copy per cell to as many as 5,300 copies per cell (5). The number of different transcripts observed in each cell population varied from 14,247 to 20,471. The bulk of the mRNA mass (75%) consisted of transcripts expressed at more than five copies per cell on average (Table 1B). In contrast, the majority (86%) of transcripts were expressed at less than 5 copies per cell, but in aggregate this low abundance class represented only 25% of the mRNA mass. This distribution was consistently observed among the different samples analyzed and was consistent with previous studies of RNA abundance classes based on RNA-DNA reassociation kinetics (Rot curves). Monte Carlo simulations revealed that our analyses had a 92% probability of detecting a transcript expressed at an average of three copies per cell (7).

Table 1 - Summary of SAGE Analysis

A. Overall Summary

	Normal		Colon		Colon		Pancreatic		Pancreatic	
	Colon	Tumors	Colon	Tumors	Cell Lines	Tumors	Colon	Tumors	Cell Lines	Total
Total Tags	62,168	60,878	60,373	61,592	58,695	303,706				
Unique Genes¹	14,721	19,690	17,092	20,471	14,247	48,741				
GenBank²	8,753 (59)	10,490 (53)	10,193 (60)	11,547 (56)	8,922 (63)	26,339 (54)				

¹ Indicates the number of different genes represented by the total tags analyzed (4).

² Indicates the number of genes that matched an entry in GenBank. The number in parentheses indicates the corresponding percentage of total unique tags.

Table 1 - Summary of SAGE Analysis

B. Summarized by Abundance Classes*

Copies/Cell	Normal		Colon		Colon		Pancreatic		Pancreatic Cell	
	Colon		Tumors		Cell Lines		Tumors		Lines	Total
> 500										
Unique Genes	62 (29)		54 (25)		54 (19)		32 (11)		70 (26)	55 (19)
GenBank	59 (95)		52 (96)		53 (98)		32 (100)		70 (100)	54 (98)
> 50 and ≤ 500										
Unique Genes	645 (28)		470 (21)		618 (27)		657 (29)		585 (27)	595 (26)
GenBank	545 (84)		429 (91)		579 (94)		609 (93)		529 (90)	553 (93)
> 5 and ≤ 50										
Unique Genes	4,569 (27)		5,011 (29)		5,733 (34)		6,146 (36)		4,895 (31)	6,209 (30)
GenBank	2,893 (63)		3,204 (64)		3,682 (64)		4,054 (66)		3,168 (65)	4,241 (68)

≤ 5						
Unique Genes	9,445 (16)	14,155 (25)	10,687 (20)	13,636 (24)	8,697 (16)	41,882 (25)
GenBank	5,256 (56)	6,805 (48)	5,879 (55)	6,852 (50)	5,155 (59)	21,491 (51)

*For unique genes, the first number denotes the number of different genes (4) represented in the indicated abundance class. The number in parentheses indicates the mass fraction (X100) of total transcripts represented by the indicated abundance class. For GenBank entries, the first number indicates the number of different genes that matched an entry in GenBank in the indicated abundance class. The number in parentheses indicates the corresponding percentage of total genes.

Many of the SAGE tags appeared to represent previously undescribed transcripts, as only 54% of the tags matched entries in GenBank (Table 1). Twenty percent of these matching transcripts corresponded to characterized mRNA sequence entries in GenBank, whereas 80% matched uncharacterized EST entries. As expected, the likelihood of a tag being present in the databases was related to abundance; GenBank matches were identified for 98% of the transcripts expressed at more than 500 copies per cell but for only 51% of the transcripts expressed at ≤ 5 copies per cell. Because the SAGE data provide a quantitative assay of transcript abundance, unaffected by differences in cloning or PCR efficiency, these data provide an independent and relatively unbiased estimate of the current completeness of publicly available EST databases.

EXAMPLE 2

This example demonstrates a comparison of the expression pattern of normal colon epithelium and primary colon cancers.

Comparison of expression patterns between normal colon epithelium and primary colon cancers revealed that the majority of transcripts were expressed at similar levels (Fig. 1A). However, the expression profiles also revealed 289 transcripts that were expressed at significantly different levels [$P < 0.01$, (8)]. Of these 289, 181 were decreased in colon tumors compared to normal colon (average decrease 10-fold; Fig. 1B; examples in Fig. 2A). Conversely, 108 transcripts were expressed at higher levels in the colon cancers than in normal colon (average increase 13-fold; Fig. 1C; examples in Fig. 2A). Monte Carlo simulations indicated that the analysis would have detected over 95% of those transcripts expressed at a 6-fold or greater level in normal vs. tumor cells or vice versa (9). Because relatively stringent criteria were used for defining differences [$P < 0.01$, (8)], the number of differences reported above is likely to be an underestimate.

EXAMPLE 3

This example demonstrates the similarities and differences between cancer cell line transcription and transcription of primary cancer tissues.

To determine how many of the 289 differences were independent of the cellular microenvironment of cancers *in vivo*, SAGE data from CR cancer cell lines was compared to that from primary CR cancer tissues (Fig. 1B, 1C). Perhaps surprisingly, the majority of transcripts (130 of 181) that were expressed at reduced levels in cancer cells *in vivo* were also expressed at significantly lower levels in the cell lines (Fig. 1B). Likewise, a significant fraction of the transcripts expressed at increased levels in primary cancers were also expressed at higher levels in the CR cancer cell lines (Fig. 1C). Thus, many of the gene expression differences that distinguish normal from tumor cells *in vivo* persist during *in vitro* growth. However, despite these similarities there were also many differences. For example, only 47 of 228 genes expressed at higher levels in CR cancer cell lines were also expressed at high levels in the primary CR cancers.

In combination, comparing the expression pattern of CR cancer cells (in *vivo* or *in vitro*) to normal colon revealed 548 differentially expressed transcripts (Fig. 1B,C, Tables 2 and 3). The average difference in expression for these transcripts was 15 fold. Although the ability to detect differences is influenced by the magnitude of the variance with the power to detect smaller differences being less, 92 transcripts that were less than three fold different were identified among the 548 transcripts. However, those genes exhibiting the greatest differences in expression are likely to be the most biologically important.

EXAMPLE 4

This example demonstrates the similarities and differences between colorectal cancer transcription and pancreatic cancer transcription.

To determine whether the changes noted in CR cancers were neoplasia or cell type specific, we performed SAGE on mRNA derived from pancreatic cancers. A total of 404 transcripts were expressed at higher levels in pancreatic cancers compared to normal colon epithelium (examples in Fig. 2B). The majority (268) of these transcripts were pancreas-specific (10) (Example in Fig. 2C) although 136 were also expressed at high levels in CR cancers. These 136 transcripts constituted 47% of the 289 transcripts increased in CR cancers relative to normal colon and are likely to be related to the neoplastic process rather than to the specific cell type of origin.

EXAMPLE 5

This example demonstrates the reproducibility of the transcription patterns observed among a larger number of cancer samples.

One question that arose from these data is the potential heterogeneity of expression between individual tumors. The SAGE data were acquired from two examples of each tissue type (normal colon, primary CR cancer, CR cancer cell line, etc.). To examine the generality of these expression profiles, we arbitrarily selected 27 differentially expressed transcripts and evaluated them in six to twelve samples of normal colon and primary cancers by Northern blot analysis (11). In general, expression patterns were very reproducible among different samples. Of 10 genes with elevated expression in normal colon relative to CR cancers as determined by SAGE, each was detected in the normal colon samples and was expressed at considerably lower levels in tumors (examples in Fig. 2A). Similarly, most of the genes identified by SAGE as increased in CR or pancreatic cancers were confirmed to be reproducibly expressed in the majority of primary cancers examined by Northern blot (examples in Fig. 2A). It is important to note, however, that there were differences among the cancers, with a few cancers exhibiting particularly high or low levels of individual transcripts. Such differences in gene expression

undoubtedly contribute to the observed heterogeneity in biological properties of cancers derived from the same organ .

EXAMPLE 6

5 This example demonstrates the identities of some of the transcripts which were found to be differentially expressed in tumor and normal tissues. What are the identities of the differentially expressed genes? Of the 548 differentially expressed transcripts, 337 were tentatively identified through database comparisons. When tested, the great majority (93%) of these identifications proved to be legitimate (13), as expected from previous SAGE
10 analyses . Although a large number of differentially expressed genes were identified, some simple patterns did emerge. For example, genes that were expressed at higher levels in normal colon epithelium than in CR tumors were often differentiation-related. These genes included liver fatty acid binding protein , cytokeratin 20 , carbonic anhydrase , guanylin and uroguanylin ,
15 which are known to be important for the normal physiology or architecture of the colon epithelium (Table 2). On the other hand, genes that were increased in CR cancers were often related to the robust growth characteristics that these cells exhibit. For example, gene products associated with protein synthesis, including 48 ribosomal proteins, five elongation factors, and five genes
20 involved in glycolysis were observed to be elevated in both CR and pancreatic cancers compared to normal colon cells. Although the majority of the transcripts could not have been predicted to be differentially expressed in cancers, several have previously been shown to be dysregulated in neoplastic cells. The latter included IGFII , B23 nucleophosmin, the Pi form of
25 glutathione S-transferase, and several ribosomal proteins which were all increased in cancer cells as previously reported. Likewise, Dra and gelsolin were both decreased in cancer as previously reported. Surprisingly, two widely studied oncogenes, *c-fos* and *c-erbB3*, were expressed at much higher levels in normal colon epithelium than CR cancers, in contrast to their up-regulation in
30 transformed cells .

In summary, these data provide basic information necessary for understanding the gene expression differences that underlie cancer phenotypes. They additionally provide a necessary framework for interpreting the significance of individual differentially expressed genes. Although this study demonstrated that a large number of such differences exist (approximately 500 at the depth of analysis employed), it was equally remarkable that the fraction of transcripts exhibiting significant differences was relatively small, representing 1.5 % of the transcripts detected in any given cell type (26). The fact that many, but not all, of the differences were preserved during in vitro culture demonstrates the utility of cultured lines for examination of some aspects of gene expression, but also provides a note of caution in relying on such lines to perfectly mimic tumors in their natural environment. Finally, the finding that hundreds of specific genes are expressed at different levels in CR cancers, and that some of these are also expressed differentially in pancreatic cancers, provides a wealth of new reagents for future biologic and diagnostic experimentation.

REFERENCES AND NOTES

1. M. D. Adams, *et al.*, *Nature* **377**, *supp.* **28**, 3 (1995); M. Schena, D. Shalon, R. W. Davis, P. O. Brown, *Science* **270**, 467 (1995); J. Derisi, *et al.*, *Nature Genetics* **14**, 457 (1996); T. M. Gress, *et al.*, *Oncogene* **13**, 1819 (1996); D. J. Lockhart, *et al.*, *Nature Biotechnology* **14**, 1675 (1996); M. Schena, *et al.*, *Proc Natl Acad Sci U S A* **93**, 10614 (1996).
2. V. E. Velculescu, L. Zhang, B. Vogelstein, K. W. Kinzler, *Science* **270**, 484 (1995); V. E. Velculescu, *et al.*, *Cell* **88**, 243 (1997).
3. To minimize individual variation, approximately equal numbers of tags (30,000) were derived from two different patients for each tissue. For primary tumors (two CR carcinomas and two pancreatic adenocarcinomas), RNA was isolated from portions of tumors judged to contain 60%-90% tumor cells by histopathology. The cells grown in vitro were derived from CR (SW837, Caco2) and pancreatic (ASPC-1, PL45) cancer cell lines. CR epithelial cells were isolated from sections of normal colon mucosa from two patients using EDTA as previously described [S. Nakamura, I. Kino, S. Baba, *Gut* **34**, 1240 (1993)]. Histopathology confirmed that the isolated cells were greater than 90% epithelial. Isolation of Poly-A RNA and SAGE was performed as previously described (2). SAGE data was analyzed by means of SAGE software and GenBank Release 95 as previously described (2).
4. A total of 69,393 different SAGE tags were identified among the 303,706 tags analyzed. A small fraction of these different tags were likely due to sequencing errors. SAGE analysis of yeast (2), wherein the entire genomic sequence is known, demonstrated a sequencing error rate of ~ 0.7%, translating to a SAGE tag error rate of 6.8% ($1 - 0.993^{10}$). Because these sequencing mistakes are essentially random, they do not substantially affect the analysis although they could artificially inflate the number of unique genes identified. Therefore, to be conservative, we reduced our estimate of unique genes identified by this maximum tag error rate (e.g., 6.8% of 303,706 total tags). The number of different tags derived from the same gene due to alternative splicing was assumed to be negligible.

5. Abundances can be simply determined by dividing the observed number of tags for a given transcript by the total number of tags obtained. An estimate of approximately 300,000 transcripts per cell was used to convert the abundances to copies per cell [N. D. Hastie, J. O. Bishop, *Cell* 9, 761 (1976)].

5 6. J. O. Bishop, J. G. Morton, M. Rosbash, M. Richardson, *Nature* 250, 199 (1974); B. Lewin, *Gene Expression Vol 2* (John Wiley and sons, New York 1980).

7. Computer simulations indicated that analysis of 300,000 tags would yield a 92 % chance of detecting a tag for a transcript whose expression was at least three copies per cell on average among the tissues examined and assuming 300,000 transcripts per cell.

8. To minimize the number of assumptions and to account for the large number of comparisons being made, Monte Carlo analysis was used for determining statistical significance. The null hypothesis was that the level, kind, and distribution of transcripts were the same for cancer and normal cells. For each transcript, 100,000 simulations were performed to determine the relative likelihood due to chance alone ("p-chance") of obtaining a difference in expression equal to or greater than the observed difference, given the null hypothesis. This likelihood was converted to an absolute probability value by simulating 40 experiments in which a representative number of transcripts (27,993 transcripts in each experiment) was identified and compared. The distribution of transcripts used for these simulations was derived from the average level of expression observed in the original samples. The distribution of the p-chance scores obtained in the 40 simulated experiments (false positives) was then compared to those obtained experimentally. Based on this comparison, a maximum value of 0.0005 was chosen for p-chance. This yielded a false positive rate that was no higher than 0.01 for the least significant p-chance value below the cutoff.

9. Two hundred simulations assuming an abundance of 0.0001 in one sample and 0.0006 in a second sample revealed a significant difference ($P < 0.01$, [8]) 95% of the time.

10. It is not possible to obtain pancreatic ductal epithelium, from which pancreatic carcinomas arise, in sufficient quantities to perform SAGE. It is therefore not possible to determine whether these transcripts were derived from genes that were highly expressed only in pancreatic cancers or were also expressed in pancreatic duct cells.
11. Total RNA isolation and Northern blot analysis was performed as described [W. S. el-Deiry, *et al.*, *Cell* **75**, 817 (1993)].
12. A. H. Owens, D. S. Coffey, S. B. Baylin, Eds., *Tumor Cell Heterogeneity: Origins and Implications* (Academic Press, New York, 1982).
13. Northern blot analyses were done on 45 of the 337 differentially expressed transcripts with tentative database matches. In three cases, the pattern of expression was not differentially expressed as predicted by SAGE and, for the purposes of this calculation, were presumed to represent incorrect database matches.
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22. G. F. Barnard, *et al.*, *Cancer Res* **52**, 3067 (1992); P. J. Chiao, D. M. Shin, P. G. Sacks, W. K. Hong, M. A. Tainsky, *Mol Carcinog* **5**, 219 (1992); N. Kondoh, C. W. Schweinfest, K. W. Henderson, T. S. Papas,

Cancer Res 52, 791 (1992); G. F. Barnard, *et al.*, *Cancer Res* 53, 4048 (1993); M. G. Denis, *et al.*, *Int J Cancer* 55, 275 (1993); J. M. Frigerio, *et al.*, *Hum Mol Genet* 4, 37 (1995).

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25. A. D. Miller, T. Curran, I. M. Verma, *Cell* 36, 51 (1984); M. H. Kraus, W. Issing, T. Miki, N. C. Popescu, S. A. Aaronson, *Proc Natl Acad Sci USA* 86, 9193 (1989).

26. In the case of normal and neoplastic colon cancer tissue, 548 differentially transcripts were identified among the 36,125 unique transcripts.

27. All references cited are hereby incorporated by reference herein.

28. Sequences tags in Tables 2-4 are consecutively numbered to form SEQ ID NOS: 1-732.

CLAIMS

1. A method of diagnosing colon cancer in a sample suspected of being neoplastic, comprising the steps of:

5 comparing the level of at least one transcript in a first sample of a tissue to a second sample, wherein the first sample is of a colonic tissue suspected of being neoplastic and the second sample is of a normal human colonic tissue, and wherein the transcript is identified by a tag selected from the group consisting of those shown in Table 3;

10 identifying the first sample as neoplastic when the level of the at least one transcript is found to be lower in the first sample than in the second sample.

2. A method of diagnosing colon cancer in a sample suspected of being neoplastic, comprising the steps of:

15 comparing the level of at least one transcript in a first sample of a tissue to a second sample, wherein the first sample is of a colonic tissue suspected of being neoplastic and the second sample is of a normal human colonic tissue, and wherein the transcript is identified by a tag selected from the group consisting of those shown in Table 2;

20 identifying the first sample as neoplastic when the level of the at least one transcript is found to be higher in the first sample than in the second sample.

3. The method of claim 1 wherein a comparison of at least two of said transcripts is performed.

25 4. The method of claim 2 wherein a comparison of at least two of said transcripts is performed.

5. The method of claim 1 wherein a comparison of at least five of said transcripts is performed.
6. The method of claim 2 wherein a comparison of at least five of said transcripts is performed.
- 5 7. The method of claim 1 wherein a comparison of at least ten of said transcripts is performed.
8. The method of claim 2 wherein a comparison of at least ten of said transcripts is performed.
- 10 9. The method of claim 1 wherein a comparison of at least twenty of said transcripts is performed.
- 10 10. The method of claim 2 wherein a comparison of at least twenty of said transcripts is performed.
11. The method of claim 1 wherein a comparison of at least thirty of said transcripts is performed.
- 15 12. The method of claim 2 wherein a comparison of at least thirty of said transcripts is performed.
13. An isolated and purified human nucleic acid molecule which comprises a SAGE tag selected from SEQ ID NO:1-732.
14. The nucleic acid molecule of claim 13 which is a cDNA molecule.

15. The nucleic acid molecule of claim 13 wherein the SAGE tag is located at the 3' end of the molecule, adjacent to the 3'-most NlaIII restriction enzyme site.
- 5 16. An isolated nucleotide probe comprising at least 10 nucleotides of a human nucleic acid molecule, wherein the human nucleic acid molecule comprises a SAGE tag selected from SEQ ID NO: 1-732.
17. The probe of claim 16 which comprises the selected SAGE tag.
18. A diagnostic reagent for evaluating neoplasia of a colorectal tissue, comprising at least 2 probes according to claim 16.
- 10 19. The diagnostic reagent of claim 18 which comprises at least 5 probes according to claim 16.
20. The diagnostic reagent of claim 18 which comprises at least 10 probes according to claim 16.
- 15 21. The diagnostic reagent of claim 18 which comprises at least 20 probes according to claim 16.
22. The diagnostic reagent of claim 18 which comprises at least 30 probes according to claim 16.
23. A diagnostic reagent for evaluating neoplasia of a colorectal tissue, comprising at least 2 probes according to claim 17.
- 20 24. A method of diagnosing pancreatic cancer in a sample suspected of being neoplastic, comprising the steps of:

comparing the level of at least one transcript in a first sample of a tissue to a second sample, wherein the first sample is of a pancreatic tissue suspected of being neoplastic and the second sample is of a normal human colon tissue, wherein said transcript is identified by a tag selected from the group consisting of those shown Table 4;

identifying the first sample as neoplastic when the level of the at least one transcript is found to be higher in the first sample than in the second sample.

25. A method of diagnosing cancer in a sample suspected of being neoplastic, comprising the steps of:

comparing the level of at least one transcript in a first sample of a tissue to a second sample, wherein the first sample is of a tissue suspected of being neoplastic and the second sample is of a normal human tissue of the same tissue type, wherein said transcript is identified by a tag selected from the group consisting of those shown Table 5;

identifying the first sample as neoplastic when the level of the at least one transcript is found to be higher in the first sample than in the second sample.

26. A method to aid in the determination of a prognosis for a colon cancer patient, comprising the steps of:

comparing the level of at least one transcript in a first sample of a tissue to a second sample, wherein the first sample is of a neoplastic colonic tissue and the second sample is of a normal human colonic tissue, and wherein the transcript is identified by a tag selected from the group consisting of those shown in Table 3;

determining a poorer prognosis if the level of the at least one transcript is found to be lower in the first sample than in the second sample.

27. A method to aid in determining a prognosis for a patient with colon cancer, comprising the steps of:

comparing the level of at least one transcript in a first tissue sample to a second sample, wherein the first sample is of a colonic cancer tissue and the second sample is of a normal human colonic tissue, and wherein the transcript is identified by a tag selected from the group consisting of those shown in Table 2;

determining a poorer prognosis if the level of the at least one transcript is found to be higher in the first sample than in the second sample.

28. A method of diagnosing colon cancer in a sample suspected of being neoplastic, comprising the steps of:

comparing the level of expression of at least one protein in a first sample of a tissue to a second sample, wherein the first sample is of a colonic tissue suspected of being neoplastic and the second sample is of a normal human colonic tissue, and wherein the protein is encoded by a transcript identified by a tag selected from the group consisting of those shown in Table 3;

identifying the first sample as neoplastic when the level of expression of the protein is found to be lower in the first sample than in the second sample.

29. A method of diagnosing colon cancer in a sample suspected of being neoplastic, comprising the steps of:

comparing the level of expression of at least one protein in a first sample of a tissue to a second sample, wherein the first sample is of a colonic tissue suspected of being neoplastic and the second sample is of a normal human colonic tissue, and wherein the protein is encoded by a transcript identified by a tag selected from the group consisting of those shown in Table 2;

identifying the first sample as neoplastic when expression of the protein is found to be higher in the first sample than in the second sample.

30. A method to aid in determining a prognosis of a patient having pancreatic cancer, comprising the steps of:

5 comparing the level of at least one transcript in a first sample of a tissue to a second sample, wherein the first sample is of a neoplastic pancreatic tissue and the second sample is of a normal human colon tissue, wherein said transcript is identified by a tag selected from the group consisting of those shown Table 4;

 determining a poorer prognosis if the level of the at least one transcript is found to be higher in the first sample than in the second sample.

10 31. A method to aid in providing a prognosis for a cancer patient, comprising the steps of:

 comparing the level of at least one transcript in a first sample of a tissue to a second sample, wherein the first sample is of a neoplastic tissue and the second sample is of a normal human tissue of the same tissue type, wherein said transcript is identified by a tag selected from the group consisting of those shown Table 5;

 determining a poorer prognosis if the level of the at least one transcript is found to be higher in the first sample than in the second sample.

20 32. A method of diagnosing pancreatic cancer in a sample suspected of being neoplastic, comprising the steps of:

 comparing the level of expression of at least one protein encoded by a transcript in a first sample of a tissue to a second sample, wherein the first sample is of a pancreatic tissue suspected of being neoplastic and the second sample is of a normal human colon tissue, wherein said protein is encoded by a transcript identified by a tag selected from the group consisting of those shown Table 4;

25 identifying the first sample as neoplastic when expression of the protein is found to be higher in the first sample than in the second sample.

33. A method of diagnosing cancer in a sample suspected of being neoplastic, comprising the steps of:

comparing the level of expression of at least one protein in a first sample of a tissue to a second sample, wherein the first sample is of a tissue suspected of being neoplastic and the second sample is of a normal human tissue, wherein said protein is encoded by a transcript identified by a tag selected from the group consisting of those shown Table 5;

identifying the first sample as neoplastic when expression of the protein is found to be higher in the first sample than in the second sample.

34. A method to aid in the determination of a prognosis for a colon cancer patient, comprising the steps of:

comparing the level of expression of at least one protein in a first sample of a tissue to a second sample, wherein the first sample is of a neoplastic colonic tissue and the second sample is of a normal human colonic tissue, and wherein the protein is encoded by a transcript identified by a tag selected from the group consisting of those shown in Table 3;

determining a poorer prognosis if the level of expression is found to be lower in the first sample than in the second sample.

35. A method to aid in determining a prognosis for a patient with colon cancer, comprising the steps of:

comparing the level of expression of at least one protein in a first tissue sample to a second sample, wherein the first sample is of a colonic cancer tissue and the second sample is of a normal human colonic tissue, and wherein the protein is encoded by a transcript identified by a tag selected from the group consisting of those shown in Table 2;

determining a poorer prognosis if the level of expression is found to be higher in the first sample than in the second sample.

36. A method to aid in determining a prognosis of a patient having pancreatic cancer, comprising the steps of:

5 comparing the level of expression of at least one protein in a first sample of a tissue to a second sample, wherein the first sample is of a neoplastic pancreatic tissue and the second sample is of a normal human colon tissue, wherein said protein is encoded by a transcript identified by a tag selected from the group consisting of those shown Table 4;

 determining a poorer prognosis if the level of expression is found to be higher in the first sample than in the second sample.

10 37. A method to aid in providing a prognosis for a cancer patient, comprising the steps of:

 comparing the level of expression of at least one protein in a first sample of a tissue to a second sample, wherein the first sample is of a neoplastic tissue and the second sample is of a normal human tissue of the same
15 tissue type, wherein said protein is encoded by a transcript identified by a tag selected from the group consisting of those shown Table 5;

 determining a poorer prognosis if the level of expression is found to be higher in the first sample than in the second sample.

20 38. A method of treating a cancer cell, comprising the step of:

 administering to a cancer cell an antibody which specifically binds to a protein encoded by a transcript identified by a tag selected from the group consisting of those shown in Tables 2, 4, and 5, wherein the antibody is linked to a cytotoxic agent.

25 39. An antibody linked to a cytotoxic agent, wherein the antibody specifically binds to a protein encoded by a transcript identified by a tag selected from the group consisting of those shown in Tables 2, 4, and 5.

40. A method of detecting colon cancer in a patient, comprising the steps of:

5 comparing the level of at least one protein in a first body sample to a second body sample, wherein the first sample is a body sample of the patient and the second sample is of a normal human, wherein the protein is encoded by a transcript identified by a tag selected from the group consisting of those shown in Table 2, wherein the first and second body sample is a sample selected from the group consisting of blood, urine, feces, sputum, and serum;

10 identifying neoplasia when the level of the at least one protein is found to be higher in the first sample than in the second sample.

41. A method of detecting pancreatic cancer in a patient, comprising the steps of:

15 comparing the level of at least one protein encoded by a transcript in a first sample of a tissue to a second sample, wherein the first sample is of the patient and the second sample is of a normal human, wherein said protein is encoded by a transcript identified by a tag selected from the group consisting of those shown Table 4, wherein the first and second sample is a sample selected from the group consisting of blood, urine, feces, sputum, and serum;

20 identifying neoplasia when the level of the at least one protein is found to be higher in the first sample than in the second sample.

42. A method of detecting cancer in a patient, comprising the steps of:

25 comparing the level of at least one protein in a first sample to a second sample, wherein the first sample is of patient and the second sample is of a normal human, wherein said protein is encoded by a transcript identified by a tag selected from the group consisting of those shown Table 5, wherein the first and second body sample is a sample selected from the group consisting of blood, urine, feces, sputum, and serum;

identifying neoplasia when the level of the at least one protein is found to be higher in the first sample than in the second sample.

43. A method to aid in determining a prognosis for a patient with colon cancer, comprising the steps of:

5 comparing the level of at least one protein in a first sample to a second sample, wherein the first sample is of a colonic cancer patient and the second sample is of a normal human, wherein the protein is encoded by a transcript identified by a tag selected from the group consisting of those shown in Table 2, wherein the first and second sample is a sample selected from the
10 group consisting of blood, urine, feces, sputum, and serum;

 determining a poorer prognosis if the level of the at least one protein is found to be higher in the first sample than in the second sample.

44. A method to aid in determining a prognosis of a patient having pancreatic cancer, comprising the steps of:

15 comparing the level of at least one protein in a first sample to a second sample, wherein the first sample is of a pancreatic cancer patient and the second sample is of a normal human, wherein said protein is encoded by a transcript identified by a tag selected from the group consisting of those shown Table 4, wherein said first and second sample is a sample selected from the
20 group consisting of blood, urine, feces, sputum, and serum;

 determining a poorer prognosis if the level of the at least one protein is found to be higher in the first sample than in the second sample.

45. A method to aid in providing a prognosis for a cancer patient, comprising the steps of:

25 comparing the level of expression of at least one protein in a first sample to a second sample, wherein the first sample is of a cancer patient and the second sample is of a normal human, wherein said protein is encoded by a transcript identified by a tag selected from the group consisting of those

shown Table 5, wherein the first and second sample is a sample selected from the group consisting of blood, urine, feces, sputum, and serum;

determining a poorer prognosis if the level of the at least one protein is found to be higher in the first sample than in the second sample.

- 5 46. A method of detecting colon cancer in a patient, comprising the steps of:

 comparing the level of at least one transcript in a first body sample to a second body sample, wherein the first sample is a body sample of the patient and the second sample is of a normal human, wherein the transcript is identified by a tag selected from the group consisting of those shown in Table 2, wherein the first and second body sample is a sample selected from the group consisting of blood, urine, feces, sputum, and serum;

 identifying neoplasia when the level of the at least one transcript is found to be higher in the first sample than in the second sample.

- 15 47. A method of detecting pancreatic cancer in a patient, comprising the steps of:

 comparing the level of at least one transcript in a first sample of a tissue to a second sample, wherein the first sample is of the patient and the second sample is of a normal human, wherein said transcript is identified by a tag selected from the group consisting of those shown Table 4, wherein the first and second sample is a sample selected from the group consisting of blood, urine, feces, sputum, and serum;

 identifying neoplasia when the level of the at least one transcript is found to be higher in the first sample than in the second sample.

- 25 48. A method of detecting cancer in a patient, comprising the steps of:

 comparing the level of at least one transcript in a first sample to a second sample, wherein the first sample is of patient and the second sample is of a normal human, wherein said transcript is identified by a tag selected

from the group consisting of those shown Table 5, wherein the first and second body sample is a sample selected from the group consisting of blood, urine, feces, sputum, and serum;

identifying neoplasia when the level of the at least one transcript is found to be higher in the first sample than in the second sample.

49. A method to aid in determining a prognosis for a patient with colon cancer, comprising the steps of:

comparing the level of at least one transcript in a first sample to a second sample, wherein the first sample is of a colonic cancer patient and the second sample is of a normal human, wherein the transcript is identified by a tag selected from the group consisting of those shown in Table 2, wherein the first and second sample is a sample selected from the group consisting of blood, urine, feces, sputum, and serum;

determining a poorer prognosis if the level of the at least one transcript is found to be higher in the first sample than in the second sample.

50. A method to aid in determining a prognosis of a patient having pancreatic cancer, comprising the steps of:

comparing the level of at least one transcript in a first sample to a second sample, wherein the first sample is of a pancreatic cancer patient and the second sample is of a normal human, wherein said transcript is identified by a tag selected from the group consisting of those shown Table 4, wherein said first and second sample is a sample selected from the group consisting of blood, urine, feces, sputum, and serum;

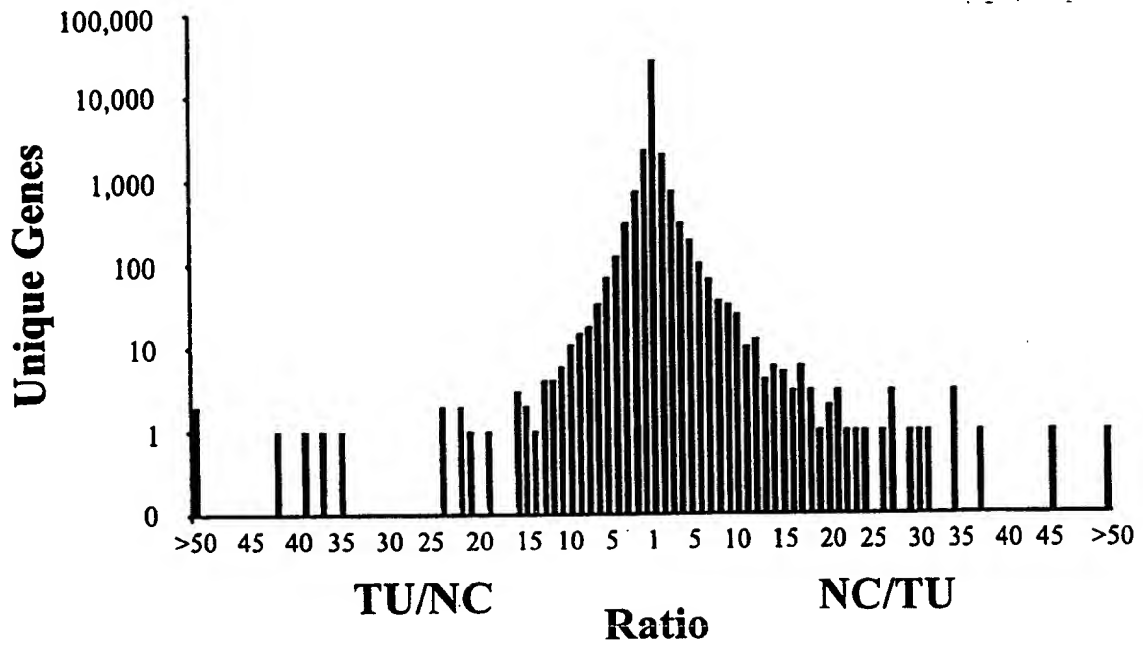
determining a poorer prognosis if the level of the at least one transcript is found to be higher in the first sample than in the second sample.

51. A method to aid in providing a prognosis for a cancer patient, comprising the steps of:

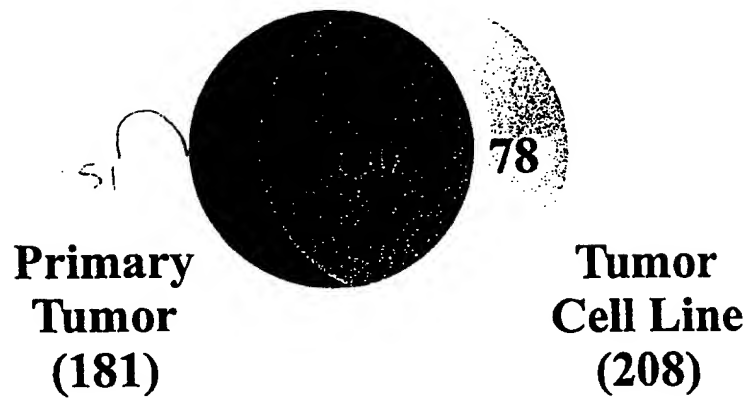
comparing the level of expression of at least one transcript in a first sample to a second sample, wherein the first sample is of a cancer patient and the second sample is of a normal human, wherein said transcript is identified by a tag selected from the group consisting of those shown Table 5, wherein the first and second sample is a sample selected from the group consisting of blood, urine, feces, sputum, and serum;

determining a poorer prognosis if the level of the at least one transcript is found to be higher in the first sample than in the second sample.

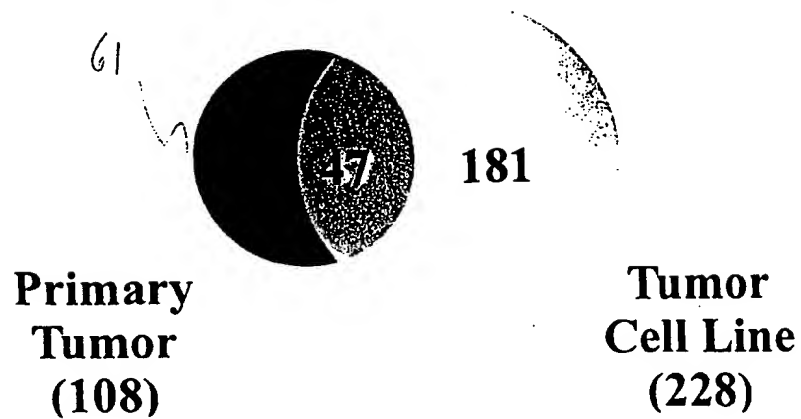
52. A method for screening for candidate agents that modulate the expression of a polynucleotide selected from the group consisting of the polynucleotides in SEQ ID NOS:1-732 or their respective complements, comprising contacting a test agent with a colon or pancreatic cell and monitoring expression of the polynucleotide, wherein the test agent which modifies the expression of the polynucleotide is a candidate agent.



B.



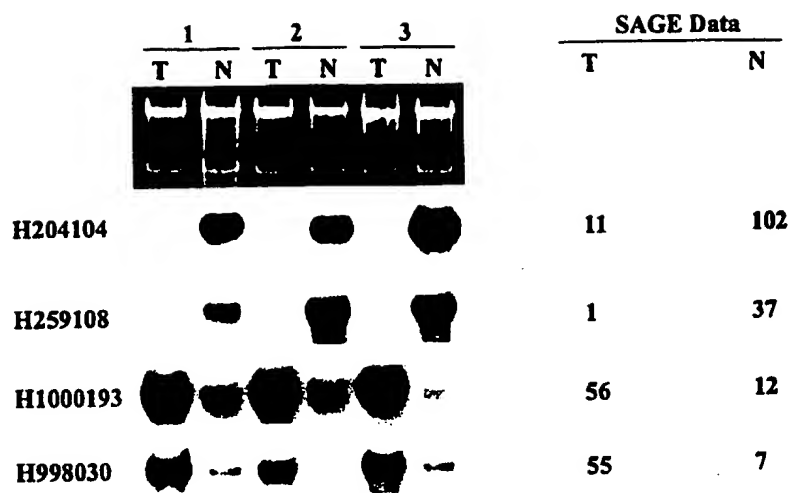
C.



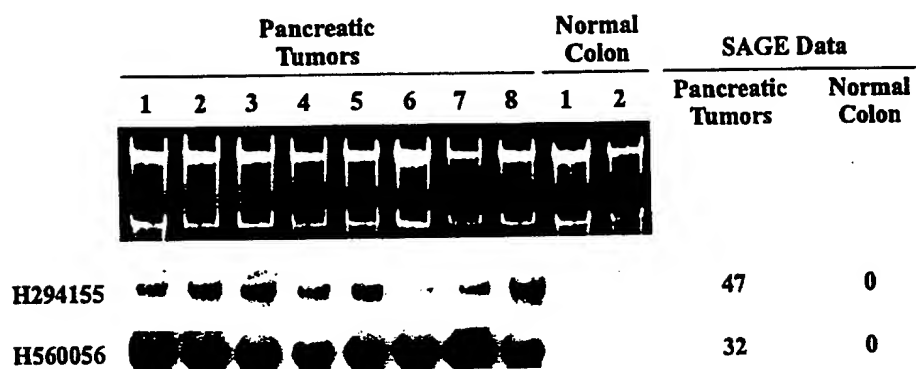
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FIG. 2

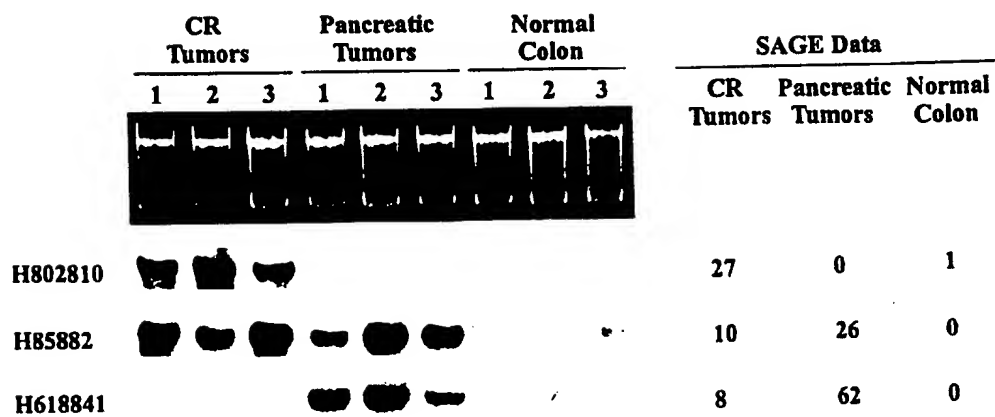
A.



B.



C.



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INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification ⁶ : C12Q 1/68, G01N 33/574	A3	(11) International Publication Number: WO 98/53319 (43) International Publication Date: 26 November 1998 (26.11.98)
(21) International Application Number: PCT/US98/10277 (22) International Filing Date: 20 May 1998 (20.05.98) (30) Priority Data: 60/047,352 21 May 1997 (21.05.97) US (63) Related by Continuation (CON) or Continuation-in-Part (CIP) to Earlier Application US 60/047,352 (CON) Filed on 21 May 1997 (21.05.97) (71) Applicant (for all designated States except US): THE JOHNS HOPKINS UNIVERSITY [US/US]; Suite 2-100, 2024 E. Monument Street, Baltimore, MD 21205 (US). (72) Inventors; and (75) Inventors/Applicants (for US only): VOGELSTEIN, Bert [US/US]; The Johns Hopkins University, Suite 2-100, 2024 E. Monument Street, Baltimore, MD 21205 (US). KINZLER, Kenneth, W. [US/US]; The Johns Hopkins University, Suite 2-100, 2024 E. Monument Street, Baltimore, MD 21205 (US).	(74) Agents: KAGAN, Sarah, A. et al.; Banner & Witcoff, Ltd., 11th floor, 1001 G Street, N.W., Washington, DC 20001-4597 (US). (81) Designated States: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, GW, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG). Published <i>With international search report.</i> <i>Before the expiration of the time limit for amending the claims and to be republished in the event of the receipt of amendments.</i> (88) Date of publication of the international search report: 8 July 1999 (08.07.99)	
(54) Title: GENE EXPRESSION PROFILES IN NORMAL AND CANCER CELLS (57) Abstract As a step towards understanding the complex differences between normal and cancer cells, gene expression patterns were examined in gastrointestinal tumors. More than 300,000 transcripts derived from at least 45,000 different genes were analyzed. Although extensive similarity was noted between the expression profiles, more than 500 transcripts that were expressed at significantly different levels in normal and neoplastic cells were identified. These data provide insights into the extent of expression differences underlying malignancy and reveal genes that are useful as diagnostic or prognostic markers.		

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EE	Estonia						

INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 98/10277

A. CLASSIFICATION OF SUBJECT MATTER

IPC 6 C12Q1/68 G01N33/574

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 6 C12Q G01N

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	SUGIO K ET AL.: "Differential expression of c-myc gene and c-fos gene in premalignant and malignant tissues." CANCER RESEARCH, vol. 48, no. 17, 1988, pages 4855-4861, XP002089885 see the whole document	1,3,13, 16,17,28
X	--- VAN BELZEN N ET AL.: "Detection of different gene expression in differentiating colon carcinoma cells by differential display" JOURNAL OF PATHOLOGY, vol. 178, no. Suppl., - 1996 page 2A XP002089886 see abstract	1,3,5,7, 9,11
Y	--- -/-	26,28,34



Further documents are listed in the continuation of box C.



Patent family members are listed in annex.

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- *L* document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
- *O* document referring to an oral disclosure, use, exhibition or other means
- *P* document published prior to the international filing date but later than the priority date claimed

T later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

X document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

Y document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

Z document member of the same patent family

Date of the actual completion of the international search

13 January 1999

Date of mailing of the international search report

24.05.1999

Name and mailing address of the ISA

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Knehr, M

INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 98/10277

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	WO 95 21944 A (SMITHKLINE BEECHAM CORP ;ROSENBERG MARTIN (US); DEBOUCK CHRISTINE) 17 August 1995 see the whole document ---	26,28,34
Y	EP 0 284 362 A (ICI PLC) 28 September 1988 see abstract see page 2, line 44 - line 51 see page 10, line 12 - line 15; claims 1,9; figure 2 ---	1,3,5,7, 9,11, 13-23, 26,28, 34,52
Y	EP 0 761 822 A (UNIV JOHNS HOPKINS MED) 12 March 1997 see the whole document ---	1,3,5,7, 9,11, 13-23, 26,28, 34,52
Y	WO 95 11923 A (DANA FARBER CANCER INST INC ;CHEN LAN BO (US); BAO SHIDENG (CN); L) 4 May 1995 see the whole document ---	1,3,5,7, 9,11, 13-18, 23,26, 28,34,52
Y	VELCULESCU V E ET AL.: "SERIAL ANALYSIS OF GENE EXPRESSION" SCIENCE, vol. 270, 20 October 1995, pages 484-487, XP002053721 cited in the application see the whole document ---	1,3,5,7, 9,11, 13-18, 23,26, 28,34,52
Y	SCHWEINFEST C W ET AL.: "Subtraction hybridization cDNA libraries from colon carcinoma and hepatic cancer" GENETIC ANALYSIS TECHNIQUES AND APPLICATIONS, vol. 7, 1990, pages 64-70, XP002089887 see the whole document ---	1,3,5,7, 9,11, 13-18, 23,26
Y	WO 97 14812 A (CHIRON CORP) 24 April 1997 see the whole document ---	52
A	GRESS T M ET AL.: "A pancreatic cancer-specific expression profile" ONCOGENE, vol. 13, 1996, pages 1819-1830, XP002089888 see the whole document ---	
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INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 98/10277

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	WO 95 19369 A (UNIV VANDERBILT) 20 July 1995 see the whole document ---	
A	GRESS T ET AL.: "Identification of genes with pancreatic cancer specific expression by use of cDNA representational difference analysis" GASTROENTEROLOGY, vol. 110, no. 4 Suppl., 1996, XP002089889 see abstract ---	
P,X	ZHANG L E AL.: "Gene expression profiles in normal and cancer cells." SCIENCE, vol. 276, 1997, pages 1268-1272, XP002089890 see the whole document ---	1,3,5,7, 9,11, 13-23, 26,28, 34,52
P,X	VAN BELZEN N ET AL.: "A novel gene which is up-regulated during colon epithelial cell differentiation and down-regulated in colorectal neoplasms" LABORATORY INVESTIGATION, vol. 77, no. 1, 1997, pages 85-92, XP002089891 see the whole document -----	1,3,5,7, 9,11,13, 14, 16-18, 23,26, 28,34

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US 98/ 10277

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☐ Claims Nos.:
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see FURTHER INFORMATION sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

see FURTHER INFORMATION sheet, subject 1.

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

International Application No. PCT/ US 98/10277

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. Claims: 1,3,5,7,9,11,13-23,26,28,34,52 (partial)

INVENTION 1:

An isolated and purified human nucleic acid molecule comprising SEQ ID NO:291 of table 3 (INVENTION 1), an isolated nucleotide probe hybridizing to it, a diagnostic reagent comprising at least two of such probes, methods of diagnosing or prognosing colon cancer using them, and a method for screening for agents modulating the expression of such a sequence using them.

2. Claims: 1,3,5,7,9,11,13-23,26,28,34,52 (partial)

INVENTION 2 to INVENTION 259:

An isolated and purified human nucleic acid molecule comprising SEQ ID NO:292 of table 3 (INVENTION 2), an isolated nucleotide probe hybridizing to it, a diagnostic reagent comprising at least two of such probes, methods of diagnosing or prognosing colon cancer using them, and a method for screening for agents modulating the expression of such a sequence using them.

...ibidem for each of the SEQ ID Nos:293 to 549 (INVENTION 3 to INVENTION 259) as specified in table 3, separately.

3. Claims: 2,4,6,8,10,12-23,27,29,35,38-40,43,46,49, 52 (partial)

INVENTION 260 to INVENTION 549:

An isolated and purified human nucleic acid molecule comprising SEQ ID NO:1 of table 2 (INVENTION 260), an isolated nucleotide probe hybridizing to it, a diagnostic reagent comprising at least two of such probes, methods of diagnosing or prognosing colon cancer using them, a method of treating a cancer cell using them, an antibody linked to a cytotoxic agent used in such a method, and a method for screening for agents modulating the expression of such a sequence using them.

...ibidem for each of the SEQ ID Nos:2 to 290 (INVENTION 261 to INVENTION 549) as specified in table 2, separately.

4. Claims: 13-24,30,32,36,38,39,41,44,47,50,52 (partial)

INTERNATIONAL SEARCH REPORT

International Application No. PCT/ US 98/10277

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

INVENTION 550 to INVENTION 732:

An isolated and purified human nucleic acid molecule comprising SEQ ID NO:550 of table 4 (INVENTION 550), an isolated nucleotide probe hybridizing to it, a diagnostic reagent comprising at least two of such probes, methods of diagnosing or prognosing pancreatic cancer using them, a method of treating a cancer cell using them, an antibody linked to a cytotoxic agent used in such a method, and a method for screening for agents modulating the expression of such a sequence using them.

...ibidem for each of the SEQ ID Nos:551 to 732 (INVENTION 551 to INVENTION 732) as specified in table 4, separately.

5. Claims: 24,30,32,36,38,39,41,44,47,50 (partial)

INVENTION 733 to INVENTION 734:

Methods of diagnosing or prognosing pancreatic cancer relying on a human nucleic acid molecule comprising SEQ ID NO:733 of table 4 (INVENTION 733), a method of treating a cancer cell using it, and an antibody linked to a cytotoxic agent used in such a method.

...ibidem for SEQ ID Nos:734 (INVENTION 734) as specified in table 4.

6. Claims: 25,31,33,37-39,42,45,48,51 (partial)

INVENTION 735 to INVENTION 870:

Methods of diagnosing or prognosing cancer relying on a human nucleic acid molecule comprising SEQ ID NO:735 of table 5 (INVENTION 735), a method of treating a cancer cell using it, and an antibody linked to a cytotoxic agent used in such a method.

...ibidem for each of the SEQ ID Nos:736 to 870 (INVENTION 736 to INVENTION 870) as specified in table 5, separately.

INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No

PCT/US 98/10277

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
WO 9521944 A	17-08-1995	EP 0743989 A JP 9508800 T	27-11-1996 09-09-1997
EP 0284362 A	28-09-1988	AU 625169 B AU 1337888 A DK 159788 A FI 881388 A JP 1034291 A PT 87055 A,B	02-07-1992 22-09-1988 24-09-1988 24-09-1988 03-02-1989 01-04-1988
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WO 9714812 A	24-04-1997	AU 7264196 A EP 0862651 A	07-05-1997 09-09-1998
WO 9519369 A	20-07-1995	US 5677125 A AU 1831795 A CA 2210396 A EP 0804453 A	14-10-1997 01-08-1995 20-07-1995 05-11-1997

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